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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:12:17 ; Search time 34.8113 Seconds  
(without alignments)  
998.335 Million cell updates

Title: US-10-088-092A-30\_COPY\_20\_142  
 Perfect score: 722  
 Sequence: 1 NLVQFGVMIEKWTGKSALQY.....YNRKYAHYPNKLCTGPTPPC 123

Scoring table: BLOSUM62

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Database : A_Geneseq_29Jan04 :
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query No.	Score	Match		Length	DB	ID	Description
			Query	Match				
1	722	100.0	142	4	AAB81022		Human pho	
2	722	100.0	154	6	ABR44235		Human sec	
3	722	100.0	154	6	ABU63125		Human gro	
4	682	91.7	142	3	AAU12810		Mouse sec	
5	662	91.7	142	4	AAAB81021		Murine pho	
6	363.5	50.3	142	6	ADA61984		Human IBM	
7	360.5	49.9	124	2	AAAR10126		Membrane-	
8	360.5	49.9	124	2	AAW73562		Human gro	
9	360.5	49.9	124	6	ADA61982		Human G72	
10	360.5	49.9	124	6	ADA61978		Human G72	
11	360.5	49.9	124	6	ABR83569		Human PLA	
12	360.5	49.9	144	1	AAAP93112		Human inf	
13	360.5	49.9	144	1	AAAP93363		Human syn	
14	360.5	49.9	144	2	AAAR25416		PLA3. 1/1	
15	360.5	49.9	144	2	ABR63055		Human PLA	
16	360.5	49.9	144	6	ABR44233		Human sec	
17	360.5	49.9	144	6	ABP96807		Human pho	
18	360.5	49.9	144	6	ABU63123		Human gro	
19	360.5	49.9	144	7	ABD75501		Prostate	
20	360.5	49.9	144	7	ADB63560		Human pro	
21	360.5	49.9	164	3	ABAS6432		Human pro	
22	357.5	48.5	124	6	ADA61983		Human T10	
23	348	48.2	125	2	AAAR63060		Rat PLA2	
24	347	48.1	146	7	ADE63558		Rat Prote	
25	341	47.2	146	2	AAW08368		Mouse PLA	

## ALIGNMENTS

RESULT 1	
AAB81022	
ID	AAB81022 standard; protein; 142 AA.
XX	
AC	AAB81022;
XX	
DT	12-JUN-2001 (first entry)
XX	
DE	Human phospholipase A2 (PLA2) amino acid sequence.

KW	Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnery;
KW	antiinflammatory; tranquiliser; antasthmatic; aniallergic; trauma;
KW	antirheumatic; antiarthritic; septic shock; pancreatitis; human;
KW	adult respiratory distress syndrome; ARDS; bronchial asthma;
KW	allergic rhinitis; rheumatoid arthritis.
XX	
XX	
OS	Homo sapiens.

Key	Location/Qualifiers
FT Peptide	1..19
FT	/label= signal_peptide
FT Protein	20..142
FT	/label= Mature_PLA2
FT	/note= "Mature phospholipase A2"

WO200121775-A1.

29-MAR-2001.

18-SEP-2000: 2000WO-JP006344.

21-SEP-1999: 99JP-00266616

(SHTO ( SHTONOCT & CO LTD

Tshizaki T. Suzuki N. Haneaki K.

WPT: 2001-290432/30

N-PSDB; AAF77401.

PT Human secretory phospholipase A2 and encoded gene, useful in diagnosis of  
PT and screening drug candidates for treating associated diseases e.g.  
PT septic shock, adult respiratory distress syndrome and rheumatoid  
PT arthritis

XX  
PS  
Claim 1: Page 46-47: 50pp: Japanese

XX  
CC This invention relates to human secretory phospholipase A2 (PLA2) protein

CC and the gene encoding it. Inhibitors of phospholipase A2 have  
CC antibacterial; immunosuppressive; anti-inflammatory; tranquilizer;  
CC vulnery; antiasthmatic; antiallergic; antirheumatic; and antiarthritic  
CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in  
CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult  
CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,  
CC allergic rhinitis and rheumatoid arthritis. The present sequence  
CC represents human PLA2  
XX  
SQ Sequence 142 AA;

Query Match 100.0%; Score 722; DB 4; Length 142;  
Best Local Similarity 100.0%; Pred. No. 8.5e-59;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLVQGVMIKMTGKSALOYNDYCYGIGGSHWPFVDTWCCHAHDCCYGRLEKLGCEP 60  
DB 20 NLVQGVMIKMTGKSALOYNDYCYGIGGSHWPFVDTWCCHAHDCCYGRLEKLGCEP 79  
QY 61 KLEKLFVSVERGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLCTGPT 120  
DB 80 KLEKLFVSVERGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLCTGPT 139

QY 121 PPC 123  
DB 140 PPC 142

RESULT 2  
ABR44235  
ID ABR44235 standard; protein; 154 AA.  
XX  
AC ABR44235;  
XX  
DT 18-AUG-2003 (first entry)  
XX  
DE Human secreted group IIE phospholipase A2 (sPLA2) enzyme.

XX Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;  
KW phosphatidylcholine; antibacterial; virucide; cytostatic; vasotropic;  
KW anti-inflammatory; vulnery; cardiant; chromosome lp35; transgenic;  
KW enzyme.

XX Homo sapiens.  
XX WO2003033689-A1.

XX 24-APR-2003.

XX 12-OCT-2001; 2001WO-IB002407.

XX 12-OCT-2001; 2001WO-IB002407.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lambeau G, Valentin E;

XX WPI; 2003-403216/38.

XX Novel mammalian secreted group IIF secreted phospholipase A2, useful for  
PT preventing and treating bacterial and viral infections, and cancers.

XX Disclosure; Fig 1; 33pp; English.

XX The invention relates to a mammalian secreted group IIF secreted  
CC phospholipase A2 (sPLA2) (1), where the enzyme is Ca2+ dependent,  
CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus  
CC phosphatidylcholine with a 15-fold preference. A pharmaceutical  
CC composition comprising (1) is useful for treating or preventing viral and  
CC bacterial infections, and cancers. A pharmaceutical composition  
CC containing compounds capable of inhibiting catalytic activity of (1),  
CC biologically active compounds that bind sPLA2 receptors, or a compound  
CC that modulates cell proliferation, cell migration, cell contraction or

CC apoptosis is useful for treating disease states or disorders involving  
CC group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain  
CC ischaemia, acute lung injury, acute respiratory distress syndrome or  
CC Crohn's disease. Specific antibodies are useful for searching new  
CC secreted mammalian group IIF sPLA2 or the homologues of the enzyme in  
CC other mammals. The encoding polynucleotides and vectors are useful for  
CC transforming animals and establishing a line of transgenic animals.  
CC Sequences ABR44232-238 represent various human secreted sPLA2 enzymes  
CC used in alignment studies with the GIIIF sPLA2 enzyme  
XX

SQ Sequence 154 AA;

Query Match 100.0%; Score 722; DB 6; Length 154;  
Best Local Similarity 100.0%; Pred. No. 9.1e-59;  
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NLVQGVMIKMTGKSALOYNDYCYGIGGSHWPFVDTWCCHAHDCCYGRLEKLGCEP 60  
DB 32 NLVQGVMIKMTGKSALOYNDYCYGIGGSHWPFVDTWCCHAHDCCYGRLEKLGCEP 91

QY 61 KLEKLFVSVERGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLCTGPT 120  
DB 92 KLEKLFVSVERGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYAHYPNKLCTGPT 151

QY 121 PPC 123  
DB 152 PPC 154

RESULT 3  
ABU63125  
ID ABU63125 standard; protein; 154 AA.

XX ABU63125;

XX 25-SEP-2003 (first entry)

XX Human group IIE secreted phospholipase A2.

XX Human; group IIE secreted phospholipase A2; virucide; antibacterial;  
KW cytostatic; anti-inflammatory; vasotropic; cerebroprotective; sPLA2;  
KW phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;  
KW viral infection; bacterial infection; cancer; inflammatory disease;  
KW cardiac ischaemia; brain ischaemia; acute lung injury;  
KW acute respiratory distress syndrome; Crohn's disease; enzyme.

XX Homo sapiens.

XX US2003073087-A1.

XX 17-APR-2003.

XX 11-OCT-2001; 2001US-00975456.

XX 11-OCT-2000; 2000US-0239491P.

XX (LAZD/) LAZDUNSKI M.

XX (LAMBEAU/) LAMBEAU G.

XX (VALE/) VALENTIN E.

XX Lazdunski M, Lambeau G, Valentin E;

XX WPI; 2003-567302/53.

XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful  
PT for treating or preventing viral or bacterial infections, or cancers, or  
PT screening inhibitors of the enzyme for treating e.g. inflammatory  
PT diseases or ischaemia.

XX Disclosure; Fig 1; 16pp; English.

XX The invention describes a mammalian secreted group IIF phospholipase A2  
CC (sPLA2), which is Ca2+-dependent, maximally active at pH of about 7-8,

CC and hydrolyses phosphatidylglycerol versus phosphatidylcholine with about  
 CC a 15-fold preference. The mammalian secreted group IIP sPLA2 protein or  
 CC nucleic acid, or a pharmaceutical composition is useful for treating  
 CC and/or preventing viral infections, bacterial infections, or cancers. The  
 CC inhibitors of sPLA2 or a composition comprising sPLA2 inhibitors is  
 CC useful for treating disease states or disorders involving group IIP  
 CC sPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia,  
 CC acute lung injury, acute respiratory distress syndrome, or Crohn's  
 CC disease. The enzyme is also useful for screening various chemical  
 CC compounds for treating these diseases. This is the amino acid sequence of  
 CC human group IIE phospholipase A2 used to determine a consensus sequence  
 CC for human sPLA2s  
 XX  
 SQ Sequence 154 AA;

Query Match 100.0%; Score 722; DB 6; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 9.1e-59;  
 Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 NLVQFGWMIERMTGKSAIQYNDYGCYCGIGSHWPVDQTDWCCHADCCYGRLEKLGCEP 60  
 DB 32 NLVQFGWMIERMTGKSAIQYNDYGCYCGIGSHWPVDQTDWCCHADCCYGRLEKLGCEP 91  
 QY 61 KLEKLVSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYKVAHYPNKLTGTPT 120  
 DB 92 KLEKLVSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYKVAHYPNKLTGTPT 151  
 QY 121 PPC 123  
 DB 152 PPC 154

RESULT 4  
 AAB12810  
 ID AAB12810 standard; protein; 142 AA.  
 AC AAB12810;  
 DT 27-NOV-2000 (first entry)  
 DE Mouse secretory type phospholipase A2 protein SEQ ID NO:15.  
 KW Mouse; secretory phospholipase A2; PLA2; screening; development;  
 KW inhibitor.  
 OS Mus musculus.  
 PN JP2000166568-A.  
 XX 20-JUN-2000.  
 XX 09-DEC-1998; 98JP-00349604.  
 XX 09-DEC-1998; 98JP-00349604.  
 XX (SHIO ) SHIONOGI & CO LTD.  
 XX WPI: 2000-485554/43.  
 DR N-PSDB; AAA73130.  
 XX  
 PT New gene encoding mouse secretory type phospholipase A2 (PLA2) for  
 PT screening for inhibitors of PLA2.  
 XX  
 PS Claim 1; Page 13-14; 15pp; Japanese.  
 CC The present invention describes a mouse secretory type phospholipase A2  
 CC (PLA2) protein. The mouse secretory type PLA2-like protein can be used  
 CC for screening in the development of inhibitors against the function of  
 CC the protein. The present sequence represents mouse secretory type PLA2  
 XX  
 SQ Sequence 142 AA;  
 Query Match 91.7%; Score 662; DB 3; Length 142;

Best Local Similarity 88.6%; Pred. No. 2.8e-53;  
 Matches 109; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 QY 1 NLVQFGWMIERMTGKSAIQYNDYGCYCGIGSHWPVDQTDWCCHADCCYGRLEKLGCEP 60  
 DB 20 NLVQFGWMIERMTGKSAIQYNDYGCYCGIGSHWPVDQTDWCCHADCCYGRLEKLGCEP 79  
 QY 61 KLEKLVSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYKVAHYPNKLTGTPT 120  
 DB 80 KLEKLVSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNRYKVAHYPNKLTGTPT 139  
 QY 121 PPC 123  
 DB 140 PPC 142

RESULT 5  
 AAB81021  
 ID AAB81021 standard; protein; 142 AA.  
 AC AAB81021;  
 DT 12-JUN-2001 (first entry)  
 DE Marine phospholipase A2 (PLA2) amino acid sequence.  
 KW Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulneryary;  
 KW antiinflammatory; tranquilliser; antiasthmatic; antiallergic; trauma;  
 KW antirheumatic; antiarthritic; septic shock; pancreatitis; mouse;  
 KW adult respiratory distress syndrome; ARDS; bronchial asthma;  
 KW allergic rhinitis; rheumatoid arthritis.  
 XX  
 OS Mus musculus.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..19  
 FT /label= Signal\_peptide  
 FT Protein 20..142  
 FT /label= Mature\_PLA2  
 FT /note= "Mature phospholipase A2"  
 XX WO200121775-A1.  
 PN 29-MAR-2001.  
 XX 18-SEP-2000; 2000WO-JP006344.  
 XX 21-SEP-1999; 99JP-00266616.  
 XX (SHIO ) SHIONOGI & CO LTD.  
 XX Ishizaki J, Suzuki N, Hanasaki K;  
 XX WPI: 2001-290432/30.  
 DR N-PSDB; AAF77387.  
 XX  
 PT Human secretory phospholipase A2 and encoded gene, useful in diagnosis of  
 PT and screening drug candidates for treating associated diseases e.g.  
 PT septic shock, adult respiratory distress syndrome and rheumatoid  
 PT arthritis.  
 XX  
 PS Example 3; Page 42; 50pp; Japanese.  
 CC This invention relates to human secretory phospholipase A2 (PLA2) protein  
 CC and the gene encoding it. Inhibitors of phospholipase A2 have  
 CC antibacterial, immunosuppressive, antiinflammatory, tranquilliser;  
 CC vulneryary; antiasthmatic; antiallergic; antirheumatic; and antiarthritic  
 CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in  
 CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult  
 CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,  
 CC allergic rhinitis and rheumatoid arthritis. The present sequence  
 CC represents murine PLA2. The murine PLA2 gene sequence is used in the  
 CC invention for the identification and characterisation of the human PLA2

CC Gene  
XX Sequence 142 AA;  
SQ

Query Match 91.7%; Score 662; DB 4; Length 142;  
Best Local Similarity 88.6%; Pred. No. 2.8e-53;  
Matches 109; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLVQFGVMIERMTGKSAIQYNDYCYGICGSGSHWPVDQTDWCCHADCCYGRLEKLGCEP 60  
DB 20 NLVQFGVMIERMTGKSAIQYNDYCYGICGSGSHWPVDQTDWCCHADCCYGRLEKLGCDP 79  
QY 61 KLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNRYAHYPNKLCTGPT 120  
DB 80 KLEKYLFSITRDNIFCAGRTACORHTCECDKRAALCFRNLGTYNRYAHYPNKLCTGPT 139  
QY 121 PPC 123  
DB 140 PPC 142

RESULT 6  
ADA61984  
ID ADA61984 standard; protein; 124 AA.  
XX ADA61984;  
AC  
DT 20-NOV-2003 (first entry)  
DE Human 18M/G72K/T103K PLA2 mutant.  
XX  
KW -Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2;  
KW group IIA PLA2; bacterial infection; Staphylococcus aureus;  
KW multi-drug resistance; wound; bloodstream infection;  
KW methicillin-resistant S. aureus; MRSA; nosocomial infection;  
KW vancomycin-resistant Enterococcus faecium; mutagen; mutant.  
XX  
OS Synthetic.  
OS Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 8  
FT /note= "Wild-type Ile substituted by Met"  
FT Misc-difference 72  
FT /note= "Wild-type Gly substituted by Lys"  
FT Misc-difference 103  
FT /note= "Wild-type Thr substituted by Lys"  
XX  
FN US6475484-B1.  
XX  
XX 05-NOV-2002.  
XX  
PF 18-DEC-2000; 2000US-00740569.  
XX  
PR 17-DEC-1999; 99US-0172467P.  
XX  
XX (UYNY ) UNIV NEW YORK STATE.  
XX  
XX Weiss J, Elsbach P, Liang N;  
XX  
DR WPI; 2003-219013/21.  
XX  
XX Treating a patient suffering from infection caused by gram-positive  
PT bacteria or killing gram-positive bacteria, comprises delivering mutant  
PT human Group IIA phospholipase A2.  
XX  
XX Example 1; Page; 22pp; English.  
PS  
XX The invention relates to killing gram-positive bacteria (I) in human  
CC patient, comprising contacting the bacteria with a bactericidal-effective  
CC amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2)  
CC appearing as ADA61978, or treating a human patient suffering from  
CC infection caused by a bacteria comprising administering a mutant human

CC Group IIA PLA2 and an antibiotic. The methods of the invention are useful  
CC for killing Gram-positive bacteria, (especially Staphylococcus aureus)  
CC and for treating human patient suffering from an infection caused by Gram  
CC -positive bacteria. The bacteria are selected from Micrococcus,  
CC Staphylococcus, Streptococcus, Peptococcus, Peptostreptococcus,  
CC Enterococcus, Methanobacterium, Bacillus, Clostridium, Lactobacillus,  
CC Listeria, Erysipelothrix, Corynebacterium, Propionibacterium,  
CC Subacterium, Actinomyces, Arachnia, Bifidobacterium, Bacterionema,  
CC Rothia, Mycobacterium, Nocardia, Streptomyces and Micropolyospora. The  
CC methods are useful for treating potentially life-threatening infection  
CC caused by multi-drug resistant Gram positive bacteria, for treating wound  
CC and bloodstream infection with methicillin-resistant S. aureus (MRSA) and  
CC nosocomial infections with vancomycin-resistant Enterococcus faecium. The  
CC present sequence represents the 18M/G72K/T103K mutant PLA2 of the  
CC invention. Note: The present sequence is not shown in the specification  
CC but was created by the indexer using the information in example 1 and the  
CC sequence appearing as ADA61978.  
XX  
SQ Sequence 124 AA;  
Query Match 50.3%; Score 363.5; DB 6; Length 124;  
Best Local Similarity 55.6%; Pred. No. 7.5e-26;  
Matches 69; Conservative 10; Mismatches 44; Indels 1; Gaps 1;

QY 1 NLVQFGVMIERMTGK-SALQYNDYCYGICGSGSHWPVDQTDWCCHADCCYGRLEKLGCE 59  
DB 1 NLVNFHRMIKLTGKEALSYGYFGCHGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60  
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNRYAHYPNKLCTGP 119  
DB 61 TFLSYKFSNSKSRITCAQDSRSQLCECDKAAATCFARNKTYNKKYQYYSNKHCRGS 120  
QY 120 TPPC 123  
DB 121 TPRC 124

RESULT 7  
AAR10126  
ID AAR10126 standard; protein; 124 AA.  
XX  
XX AAR10126;  
AC  
DT 25-MAR-2003 (revised)  
DT 19-MAR-1991 (first entry)  
XX  
XX Membrane-bound phospholipase A2 from human spleen.  
XX  
XX human phospholipase A2; anti-inflammatory drugs.  
XX  
XX Homo sapiens.  
XX  
XX JP02286081-A.  
XX  
PD 26-NOV-1990.  
XX  
PF 27-APR-1989; 89JP-00110269.  
XX  
XX 27-APR-1989; 89JP-00110269.  
XX  
XX (SHIO ) SHIONOGI & CO LTD.  
XX  
XX WPI; 1991-012217/02.  
XX  
XX Human spleen deriving membrane bound phospholipase A2 - used for  
PT screening antiinflammatory drug.  
PT  
XX  
XX Claim 2; Page 1; 6pp; Japanese.  
PS  
XX Human spleen was homogenated then centrifuged to obtain a precipitated  
CC pellet comprising the cell membrane component. The pellet was extracted  
CC with KBr aq. solution. Pure phospholipase A2 was obtained from the crude  
CC preparation by a combination of chromatography techniques. The protein

CC can be used as an antigen to generate monoclonal antibodies with  
 CC specificity against human spleen- derived phospholipase A2. The  
 CC monoclonal antibodies can be used in the diagnosis of inflammation.  
 CC (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 124 AA;

Query Match 49.9%; Score 360.5; DB 2; Length 124;  
 Best Local Similarity 55.6%; Pred. No. 1.4e-25;  
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;  
 XX  
 SQ Sequence 124 AA;

QY 1 NLVQFGVMIEKMTGK-SALOYNDYGCYGGSHWPVDQTDWCHAHDCYGRLEKLGCE 59  
 DB 1 NLVNFHRMILKTGKEAALSFGYGHGCGVGRGSPKDATDRCCVTHDCYKRLKRGCG 60  
 QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTNNRYAHYPNKLCTGP 119  
 DB 61 TKFLSYKFSNSGRITCAKQDSCRSCQCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 120  
 QY 120 TPPC 123  
 DB 121 TPRC 124

RESULT 8  
 AAW73562  
 ID AAW73562 standard; protein; 124 AA.  
 XX  
 AC AAW73562;  
 XX  
 DT 10-MAR-1999 (first entry)  
 XX  
 DE Human group II secretory phospholipase A2 protein.  
 XX  
 KW Human group II secretory phospholipase A2; hspLA2 grII; Fxa inhibitor;  
 KW coagulation disorder; haemostatic disorder; Fva/Fva complex formation;  
 KW therapy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO985504-A1.  
 XX  
 PD 10-DEC-1998.  
 XX  
 PF 04-JUN-1998; 98WO-IB000869.  
 XX  
 PR 05-JUN-1997; 97US-0048668P.  
 XX  
 PA (INSP ) INST PASTEUR.  
 XX  
 PI Mounier C, Hackeng T, Griffin J, Bon C;  
 XX  
 DR WPI; 1999-045729/04.  
 XX  
 PT New peptide fragment of human group II secretory phospholipase A2 (hsPLA2  
 PT grII) - useful in the treatment or prevention of coagulation and  
 PT hemostatic disorders.  
 XX  
 PS Example 6; Page 27; 62pp; English.

This sequence represents the full length human group II secretory  
 phospholipase A2 (hsPLA2 grII) protein. The invention relates to peptides  
 comprising eleven amino acids, corresponding to residues 51-62 of hsPLA2  
 grII. The peptides are useful in screening new compounds for their  
 potential use as drugs in the treatment or prevention of coagulation  
 disorders (particularly thrombus formation and limiting platelet  
 activation in vivo in humans and animals). The peptides and antibodies  
 form compositions in the regulation of the coagulant effect in vivo in  
 humans or animals. The peptides are also useful, in forming kits in the  
 detection of haemostatic disorders. Additionally, the peptides and  
 antibodies form compositions in the treatment or prevention of  
 haemostatic disorders. The peptide represents the specific region of  
 hsPLA2 grII involved in the inhibition of the Fva/Fva complex formation,

CC and Fxa inhibition, which maximizes the effects of drugs based on the  
 CC peptide  
 XX  
 SQ Sequence 124 AA;

Query Match 49.9%; Score 360.5; DB 2; Length 124;  
 Best Local Similarity 55.6%; Pred. No. 1.4e-25;  
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;  
 XX  
 SQ Sequence 124 AA;

QY 1 NLVQFGVMIEKMTGK-SALOYNDYGCYGGSHWPVDQTDWCHAHDCYGRLEKLGCE 59  
 DB 1 NLVNFHRMILKTGKEAALSFGYGHGCGVGRGSPKDATDRCCVTHDCYKRLKRGCG 60  
 QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTNNRYAHYPNKLCTGP 119  
 DB 61 TKFLSYKFSNSGRITCAKQDSCRSCQCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 120  
 QY 120 TPPC 123  
 DB 121 TPRC 124

RESULT 9  
 ADA61982  
 ID ADA61982 standard; protein; 124 AA.  
 XX  
 AC ADA61982;  
 XX  
 DT 20-NOV-2003 (first entry)  
 XX  
 DE Human G72K PLA2 mutant.  
 XX  
 KW Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2;  
 KW group IIA PLA2; bacterial infection; Staphylococcus aureus;  
 KW multi-drug resistance; wound; bloodstream infection;  
 KW methicillin-resistant S. aureus; MRSA; nosocomial infection;  
 KW vancomycin-resistant Enterococcus faecium; murein; mutant.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Misc-difference 72 /note= "Wild-type Gly substituted by Lys"  
 XX  
 FT US6475484-B1.  
 XX  
 PD 05-NOV-2002.  
 XX  
 PF 18-DEC-2000; 2000US-00740569.  
 XX  
 PR 17-DEC-1999; 99US-0172467P.  
 XX  
 PA (UUNY ) UNIV NEW YORK STATE.  
 XX  
 PI Weiss J, Elsbach P, Liang N;  
 XX  
 DR WPI; 2003-219013/21.  
 XX  
 PT Treating a patient suffering from infection caused by gram-positive  
 PT bacteria or killing gram-positive bacteria, comprises delivering mutant  
 PT human Group IIA phospholipase A2.  
 XX  
 PS Example 1; Page; 22pp; English.

The invention relates to killing gram-positive bacteria (I) in human  
 patient, comprising contacting the bacteria with a bactericidal-effective  
 amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2)  
 appearing as ADA61978, or treating a human patient suffering from  
 infection caused by a bacteria comprising administering a mutant human  
 Group IIA PLA2 and an antibiotic. The methods of the invention are useful  
 for killing Gram-positive bacteria, (especially Staphylococcus aureus)  
 and for treating human patient suffering from an infection caused by Gram

CC -positive bacteria. The bacteria are selected from Micrococcus,  
 CC Staphylococcus, Streptococcus, Peptococcus, Peptostreptococcus,  
 CC Enterococcus, Methanobacterium, Bacillus, Clostridium, Lactobacillus,  
 CC Listeria, Erysipelothrix, Corynebacterium, Propionibacterium,  
 CC Eubacterium, Actinomyces, Arachnia, Bifidobacterium, Bacterionema, The  
 CC Eubacterium, Mycobacterium, Nocardia, Streptomyces and Micropolytopora. The  
 CC methods are useful for treating potentially life-threatening infection  
 CC caused by multi-drug resistant Gram positive bacteria, for treating wound  
 CC and bloodstream infection with methicillin-resistant S. aureus (MRSA) and  
 CC nosocomial infections with vancomycin-resistant Enterococcus faecium. The  
 CC present sequence represents the G72K mutant PLA2 of the invention. Note:  
 CC the present sequence is not shown in the specification but was created by  
 CC the indexer using the information in example 1 and the sequence appearing  
 CC as ADA61978.  
 XX  
 SQ Sequence 124 AA;  
 Query Match 49.9%; Score 360.5; DB 6; Length 124;  
 Best Local Similarity 54.8%; Pred. No. 1.4e-25;  
 Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;  
 QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGGSHWPDQTDWCCHADCCYGRLEKLGCE 59  
 Db 1 NLVNFHRLIKLTTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60  
 QY 60 PKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNKYAHYPNKLCTGP 119  
 Db 61 TKFLSYKFSNSKRITCAKQDSCRSQLECDKAAATCFARNKTYNKKYQYVSNHCRGS 120  
 QY 120 TPPC 123  
 Db 121 TPRC 124  
 RESULT 10  
 ADA61978  
 ID -ADA61978 standard; protein; 124 AA.  
 AC ADA61978;  
 XX 20-NOV-2003 (first entry)  
 DT Human G72K/Ti03K PLA2 mutant.  
 DE  
 XX Antibacterial; gram-positive bacteria; human; group IIA phospholipase A2;  
 KW group IIA PLA2; bacterial infection; Staphylococcus aureus;  
 KW multi-drug resistance; wound; bloodstream infection;  
 KW methicillin-resistant S. aureus; MRSA; nosocomial infection;  
 KW vancomycin-resistant Enterococcus faecium; muten; mutant.  
 XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 FH Key  
 FT Misc-difference 72  
 FT /note= "Wild-type Gly substituted by Lys"  
 FT Misc-difference 103  
 FT /note= "Wild-type Thr substituted by Lys"  
 FT  
 XX US6475484-B1.  
 FN  
 XX 05-NOV-2002.  
 PD  
 XX 18-DEC-2000; 2000US-00740569.  
 XX  
 XX 17-DEC-1999; 95US-0172467P.  
 PR  
 XX (UNNY ) UNIV NEW YORK STATE.  
 PA Weiss J, Elsbach P, Liang N;  
 XX WPI; 2003-219013/21.  
 PI N-PSDB; ADA61977.  
 DR  
 DR

XX Treating a patient suffering from infection caused by gram-positive  
 PT bacteria or killing gram-positive bacteria, comprises delivering mutant  
 PT human Group IIA phospholipase A2.  
 XX Claim 1; Fig 3; 22pp; English.  
 PS  
 XX The invention relates to killing gram-positive bacteria (I) in human  
 CC patient, comprising contacting the bacteria with a bactericidal-effective  
 CC amount of mutant human Group IIA phospholipase A2 (Group IIA PLA2)  
 CC appearing as ADA61978, or treating a human patient suffering from  
 CC infection caused by a bacteria comprising administering a mutant human  
 CC Group IIA PLA2 and an antibiotic. The methods of the invention are useful  
 CC for killing Gram-positive bacteria, (especially Staphylococcus aureus)  
 CC and for treating human patient suffering from an infection caused by Gram  
 CC -positive bacteria. The bacteria are selected from Micrococcus,  
 CC Staphylococcus, Streptococcus, Peptococcus, Peptostreptococcus,  
 CC Enterococcus, Methanobacterium, Bacillus, Clostridium, Lactobacillus,  
 CC Listeria, Erysipelothrix, Corynebacterium, Propionibacterium,  
 CC Eubacterium, Actinomyces, Arachnia, Bifidobacterium, Bacterionema,  
 CC Rothia, Mycobacterium, Nocardia, Streptomyces and Micropolytopora. The  
 CC methods are useful for treating potentially life-threatening infection  
 CC caused by multi-drug resistant Gram positive bacteria, for treating wound  
 CC and bloodstream infection with methicillin-resistant S. aureus (MRSA) and  
 CC nosocomial infections with vancomycin-resistant Enterococcus faecium. The  
 CC present sequence represents the G72K/Ti03K mutant PLA2 of the invention.  
 XX  
 SQ Sequence 124 AA;  
 Query Match 49.9%; Score 360.5; DB 6; Length 124;  
 Best Local Similarity 54.8%; Pred. No. 1.4e-25;  
 Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;  
 QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGGSHWPDQTDWCCHADCCYGRLEKLGCE 59  
 Db 1 NLVNFHRLIKLTTGKEAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60  
 QY 60 PKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRRNLGTYNKYAHYPNKLCTGP 119  
 Db 61 TKFLSYKFSNSKRITCAKQDSCRSQLECDKAAATCFARNKTYNKKYQYVSNHCRGS 120  
 QY 120 TPPC 123  
 Db 121 TPRC 124  
 RESULT 11  
 ABR83569  
 ID ABR83569 standard; protein; 124 AA.  
 XX  
 AC ABR83569;  
 XX 14-OCT-2003 (first entry)  
 DT  
 XX Human PLA2 amino acid sequence SEQ ID NO:36.  
 DE Fusion protein; Tola; TolAII domain; bor; Escherichia coli; human;  
 KW interaction; cleavage site.  
 KW  
 XX Homo sapiens.  
 OS  
 XX WO2003057708-A2.  
 FN  
 XX 17-JUL-2003.  
 PD  
 XX 10-JAN-2003; 2003WO-GB0000078.  
 PF  
 XX 10-JAN-2002; 2002GB-00000689.  
 PR  
 XX (UYNE-) UNIV NEWCASTLE VENTURES LTD.  
 PA Gokce I, Anderlueh G, Lakey JH;  
 PI  
 XX

DR WPI; 2003-587105/55.  
XX New fusion polypeptides, useful for immobilization or purification and  
XX isolation of the non-Tola polypeptide, or for studying interaction  
PT properties of the non-Tola polypeptide or the fusion polypeptide, e.g.  
PT self-interaction.  
XX  
XX Example 1; Page 56-57; 68pp; English.  
XX  
XX The present invention describes a fusion polypeptide (I) for expression  
XX in a host cell comprising a TolAIII domain (functional homologue,  
XX fragment or derivative), and a non-Tola polypeptide, where the TolAIII  
XX domain (functional homologue, fragment or derivative) is located towards  
XX the N-terminus of the fusion polypeptide, and the non-Tola polypeptide is  
XX located towards the C-terminus of the fusion polypeptide. Also described:  
XX (1) a DNA molecule (II) encoding the fusion polypeptide (I); (2) an  
XX expression vector (III) comprising the fusion polypeptide (I); (3) a  
XX cloning vector (IV) for producing the expression vector comprising DNA  
XX (II) encoding the TolAIII domain (functional homologue, fragment or  
XX derivative) upstream or downstream from a cloning site which allows in-  
XX frame insertion of DNA encoding a non-Tola polypeptide; and (4) a host  
XX cell containing (II), and/or (III), and/or (IV). The TolAIII domain  
XX (functional homologue, fragment or derivative) is useful for producing  
XX the fusion polypeptide (I), DNA molecule (II), expression vector (III) or  
XX cloning vector (IV). The fusion polypeptide (I) is useful for  
XX immobilization or purification and isolation of the non-Tola polypeptide,  
XX or for studying interaction properties of the non-Tola polypeptide or the  
XX fusion polypeptide, e.g. self-interaction, interaction with another  
XX molecule or interaction with a physical stimulus and for high expression  
XX of a polypeptide as a fusion polypeptide in a host cell. ACF57145 to  
XX ACF57176 and ABR83541 to ABR83574 represent sequence used in the  
XX exemplification of the present invention  
XX  
XX Sequence 124 AA;  
XX  
XX Query Match 49.9%; Score 360.5; DB 6; Length 124;  
XX Best Local Similarity 55.6%; Pred. No. 1.4e-25;  
XX Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;  
XX  
QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGGGHWPVDQTDWCCHADCCYGRLEKLGCE 59  
Db 1 NLVNFHFMILTTGKEALSYGFYGCYGGGSPKDATDRCCVTHDCCYKLEKRGCG 60  
QY 60 PLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRNLCTYNRKYAHYPNKLCTGP 119  
Db 61 TKELSYKFSNGSRITCAKQDSRSQLCECDKRAANTCFARKTYNKKYQYFNKHCGRGS 120  
QY 120 TPCC 123  
Db 121 TPRC 124  
XX  
RESULT 12  
AAP93112  
XX AAP93112 standard; protein; 144 AA.  
XX AAP93112;  
XX  
XX 25-MAR-2003 (revised)  
DT 31-JUL-1992 (first entry)  
XX  
XX Human inflammatory phospholipase A2 encoded by HindIII fragment of PLA2  
DE 8.5 EMBL3.  
XX  
XX Inflammation; acid stable; phosphatide 2-acylhydrolase; lipolytic;  
KW glycerophospholipids; non-pancreatic.  
XX  
XX Homo sapiens.  
XX  
XX Key Location/Qualifiers  
FH Peptide 1..20  
FT /label= signal  
FT 1..14  
FT Region

FT Region /label= exon\_1  
FT 15..62  
FT /label= exon\_2  
FT 21..39  
FT /note= "Claim 12"  
FT 22..37  
FT /note= "Claim 14"  
FT 44..56  
FT /note= "calcium binding loop"  
FT 63..98  
FT /label= exon\_3  
FT 67  
FT Active-site  
FT Binding-site  
FT 68  
FT Active-site  
FT 71  
FT Active-site  
FT 86  
FT Region 99..124  
FT /label= exon\_4  
FT 111  
XX  
XX WO8909818-A.  
PN  
XX 19-OCT-1989.  
PD  
XX 11-APR-1989; 89WO-US001418.  
XX  
XX 15-APR-1988; 88US-00181893.  
PR  
XX 12-JUL-1988; 88US-00219491.  
XX  
XX (BIOJ ) BIOGEN INC.  
PA  
XX  
XX Kramer RM, Pepinsky R, Hession C;  
PI  
XX WPI; 1989-324225/44.  
XX  
XX N-PSDB; AAN91825, AAN97209.  
DR  
XX  
XX Acid stable phospholipase A2 - used for prodn. of antibodies and in the  
PT treatment or diagnosis of inflammation and other diseases.  
XX  
XX Claim 44; Fig 12; 84pp; English.  
PS  
XX  
XX The protein sequence was deduced from a DNA sequence obtd. from a genomic  
CC DNA library which was prepd. from a mutant fibroblast cell line which  
CC contains 5 copies of the X chromosome (GM5009). The signal sequence is  
CC thought to be incomplete at the N-terminal since no promoter-like  
CC sequences are found in the DNA within 100 nucleo- tides 5' of this  
CC region. The deduced N-terminal sequence of the mature protein confirmed  
CC results obtd. by direct sequencing of the purified protein. This sequence  
CC represents an amphiphilic alpha- helix typical of PLA 2 mols. It has  
CC highly conserved lipophilic residues [e.g. Leu (22), Phe (25), and Ile  
CC (29)] and there is a cluster of basic amino acids [e.g. Arg (27), Lys  
CC (30) and Lys (35)] which is believed to be an important determinant in  
CC the interaction of PLA 2. There is a characteristic stretch of residues  
CC which comprises part of the calcium binding loop: Tyr(44)-Gly-X-Cys-  
CC Gly-X-Gly-X-X-X-Pro(56) and Asp(58). The conserved residues which  
CC constitute the active site (see features) are also present, and the  
CC protein exhibits the placement of half-cysteine residues typical of a Gp  
CC II PLA 2, having a Cys residue at position 70 and a half cysteine at the  
CC C-terminal. (The consensus sequence was determined from a comparison of  
CC PLA 2s from bovine pancreas and C. atrox venom. (Updated on 25-MAR-2003  
CC to correct PR field.)  
XX  
XX Sequence 144 AA;  
SQ

Query Match 49.9%; Score 360.5; DB 1; Length 144;  
Best Local Similarity 55.6%; Pred. No. 1.6e-25;  
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;  
QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGGGHWPVDQTDWCCHADCCYGRLEKLGCE 59  
Db 21 NLVNFHFMILTTGKEALSYGFYGCYGGGSPKDATDRCCVTHDCCYKLEKRGCG 80  
QY 60 PLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRNLCTYNRKYAHYPNKLCTGP 119

```

Db      81 TKFLSYKFSNSGSRITCAKQDSCRSQSCDCAAAATCFARNKTTYNKKYQYYSNKHCRGS 140
QY      120 TPPC 123
Db      141 TPRC 144

RESULT 13
AAP93363
ID AAP93363 standard; protein; 144 AA.
XX AC AAP93363;
XX DT 25-MAR-2003 (revised)
XX DT 27-JUN-1980 (first entry)
XX DE Human synovial phospholipase type A2 (sPLA2) as encoded by cDNA clone
XX DE lambda SPLA2cDNA-4 and by the exons of clone lambda SPLA2-6.
XX KW Human synovial phospholipase A2; clone lambda SPLA2cDNA-4;
XX KW lambda SPLA2-6.
XX OS Homo sapiens.
XX FT Key Location/Qualifiers
XX FT Protein 21..144
XX PN WO8901773-A.
XX PD 09-MAR-1989.
XX PF 23-AUG-1988; 88WO-US002896.
XX PR 27-AUG-1987; 87US-00089883.
XX PR 06-JUL-1988; 88US-00215726.
XX PR 16-AUG-1988; 88US-00231865.
XX PA (BIOT-) BIOTECHN RES PARTN.
XX PA (UTOR) UNIV OF TORONTO INNOVAT.
XX PI Johnson LK, Seilhamer JJ, Pruzanski W, Vadas P;
XX WPI; 1989-085394/11.
XX DR N-PSDB; AAN91258, AAN91260.
XX CC Mammalian synovial phospholipase A2 - used in food processing, design and
XX CC screening of inflammation inhibitors, as an anticancer drug or vaccine
XX CC adjuvant etc.
XX PS Disclosure; Fig 6; 70pp; English.
XX CC Clone lambda SPLA2cDNA-4 is one of four clones identified when probe
XX CC oligo 2905 (AAN91257) was used to screen a cDNA library constructed from
XX CC polyA+ message from a peritoneal cell RNA. It encodes the entire sPLA2
XX CC type A sequence which is given here. The mature peptide sequence (see FT)
XX CC has a calculated molecular weight of 13,919 daltons. The same amino acid
XX CC sequence is also encoded by the exons of clone lambda SPLA2-6 (AAN91260)
XX CC in Figure 7. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25
XX CC -MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI
XX CC field.)
SQ      Sequence 144 AA;
Query Match 49.9%; Score 360.5; DB 1; Length 144;
Best Local Similarity 55.6%; Pred. No. 1.6e-25;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY      1 NLVQFVMIKWTGK-SALQYNDYGCYIGGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
Db      21 NLVNFHRMIKLTGKGAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 80
QY      60 PKLEKYLFSVSEGRIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGP 119
Db      81 TKFLSYKFSNSGSRITCAKQDSCRSQSCDCAAAATCFARNKTTYNKKYQYYSNKHCRGS 140
QY      120 TPPC 123
Db      141 TPRC 144

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Db      81 TKFLSYKFSNSGSRITCAKQDSCRSQSCDCAAAATCFARNKTTYNKKYQYYSNKHCRGS 140
QY      120 TPPC 123
Db      141 TPRC 144

RESULT 14
AAR25416
ID AAR25416 standard; protein; 144 AA.
XX AC AAR25416;
XX DT 06-JAN-1993 (first entry)
XX DE PLA2.
XX KW Human growth hormone; granulocyte-colony stimulating factor; G-CSF;
XX KW phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy;
XX KW erythroid cells; cDNA library.
XX OS Synthetic.
XX PN GB2251622-A.
XX PD 15-JUL-1992.
XX PF 19-DEC-1991; 91GB-00026984.
XX PR 21-DEC-1990; 90GB-00027917.
XX PA (ICIL) IMPERIAL CHEM IND PLC.
XX PI Hollis M, Needham MRC, Gooding C, Grosveld FG, Antoniou M;
XX WPI; 1992-236158/29.
XX DR N-PSDB; AAQ26372.
XX PT Expression vectors for use in mammalian cells - contain dominant control
XX PT region derived from beta-globin gene.
XX PS Disclosure; Fig 11; 77pp; English.
XX CC This sequence is encoded by the phospholipase A2 (PLA2) cDNA. The cDNA
XX CC was amplified using the primer sequences given in AAQ26370-1 by PCR from
XX CC a human lung cDNA library. The cDNA sequence was used in the construction
XX CC of an expression vector which further comprised a promoter and a dominant
XX CC control region. This vector was used in an expression system comprising a
XX CC mammalian cell transformed with the vector. This expression system could
XX CC be used to prepare pharmacologically useful polypeptides eg. human growth
XX CC hormone (HGH), granulocyte-colony stimulating factor (G-CSF) and PLA2,
XX CC and for gene therapy. The mammalian host comprises erythroid cells and a
XX CC heterologous promoter
XX CC Sequence 144 AA;
SQ      Query Match 49.9%; Score 360.5; DB 2; Length 144;
Best Local Similarity 55.6%; Pred. No. 1.6e-25;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY      1 NLVQFVMIKWTGK-SALQYNDYGCYIGGSHWPVDQTDWCCHADCCYGRLEKLGCE 59
Db      21 NLVNFHRMIKLTGKGAALSYGFYCHGCGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 80
QY      60 PKLEKYLFSVSEGRIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTGP 119
Db      81 TKFLSYKFSNSGSRITCAKQDSCRSQSCDCAAAATCFARNKTTYNKKYQYYSNKHCRGS 140
QY      120 TPPC 123
Db      141 TPRC 144

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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:17:51 ; Search time 43.6302 Seconds  
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877.555 Million cell updates/sec

Title: US-10-088-092a-30\_COPY\_20\_142

Perfect score: 722

Sequence: 1 NLVQGVMIERWTKSALQY.....YNRKYAHYPNKLCTGTPPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1276540 seqs, 311283816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	100.0	154	10	US-09-975-456B-8
2	360.5	49.9	124	14	US-10-255-576-2
3	360.5	49.9	144	10	US-09-975-456B-6
4	360.5	49.9	144	14	US-10-203-823-325
5	360.5	49.9	144	15	US-10-116-275-269
6	360.5	49.9	164	9	US-09-925-300-1010
7	341	47.2	341	8	US-09-993-999-8
8	341	47.2	146	13	US-10-124-591-3
9	337	46.7	146	13	US-10-124-591-4
10	335.5	46.5	138	12	US-09-917-805-7
11	330.5	45.8	138	12	US-09-917-805-6
12	311.5	43.1	138	12	US-09-917-805-2
13	303	42.0	168	10	US-09-975-456B-2
14	303	42.0	168	15	US-10-104-047-3735
15	303	42.0	211	14	US-10-345-680-23

16	303	42.0	211	15	US-10-295-027-195
17	303	42.0	211	16	US-10-278-938-2
18	303	42.0	211	16	US-10-188-832-80
19	299.5	41.5	118	9	US-09-987-655-5
20	299.5	41.5	118	9	US-09-987-675-5
21	299.5	41.5	118	10	US-09-975-456B-9
22	292.5	40.5	145	9	US-09-969-384-17
23	292.5	40.5	145	10	US-09-975-456B-7
24	290.5	40.2	145	9	US-09-835-968A-6
25	290.5	40.2	150	12	US-10-296-115-1342
26	288.5	40.0	137	9	US-09-993-999-9
27	287.5	39.8	155	10	US-09-975-456B-10
28	287.5	39.8	165	13	US-10-124-591-1
29	270.5	37.5	145	12	US-09-917-805-9
30	265	36.7	145	12	US-09-917-805-4
31	249	34.5	145	12	US-09-917-805-5
32	227.5	31.5	145	12	US-09-917-805-8
33	226.5	31.4	148	10	US-09-975-456B-5
34	226.5	31.4	148	12	US-09-917-805-3
35	226.5	31.4	156	9	US-09-925-297-511
36	225.5	31.2	146	12	US-09-917-805-1
37	216	29.9	146	9	US-09-993-999-7
38	200	27.7	151	12	US-10-338-663-7
39	198.5	27.5	152	14	US-10-230-058A-15
40	193.5	26.8	133	15	US-10-371-725-7
41	186	25.8	143	9	US-09-993-999-10
42	178	24.7	153	15	US-10-369-493-5548
43	175	24.2	116	10	US-09-946-374-378
44	175	24.2	116	12	US-10-147-493-534
45	175	24.2	116	12	US-10-145-127-534

#### ALIGNMENTS

#### RESULT 1

US-09-975-456B-8  
; Sequence 8, Application US/09975456B  
; Publication NO. US20030073087A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; APPLICANT: LAMBEAU, GERARD  
; APPLICANT: VALENTIN, EMMANUEL  
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2  
; FILE REFERENCE: 1478-R-00  
; CURRENT APPLICATION NUMBER: US/09/975,456B  
; PRIOR FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: 60/239,491  
; PRIOR FILING DATE: 2000-10-11  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 2.1  
; SEQ ID NO 8  
; LENGTH: 154  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-975-456B-8

Query Match	100.0%	Score	722	DB	10	Length	154
Best Local Similarity	100.0%	Pred. No.	7e+72				
Matches	123	Conservative	0	Mismatches	0	Indels	0
Gaps	0						
Qy	1	NLVQGVMIERWTKSALQYNDYGCYGGIGGSHWPVQTDWCCHAHDCCYGRLEKLGCEP	60				
Db	32	NLVQGVMIERWTKSALQYNDYGCYGGIGGSHWPVQTDWCCHAHDCCYGRLEKLGCEP	91				
Qy	61	KLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTVNRKYAHYPNKLCTGPT	120				
Db	92	KLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTVNRKYAHYPNKLCTGPT	151				
Qy	121	PPC 123					
Db	152	PPC 154					

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RESULT 2
US-10-255-576-2
; Sequence 2, Application US/10255576
; Publication No. US20030161822A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Jerrold
; APPLICANT: Elsbach, Peter
; APPLICANT: Liang, Ning-Sheng
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
; FILE REFERENCE: 5986/1E917U51
; CURRENT APPLICATION NUMBER: US/10/255,576
; CURRENT FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: US/09/740,569
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/172,467
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-255-576-2
Query Match 49.9%; Score 360.5; DB 14; Length 124;
Best Local Similarity 54.8%; Pred. No. 5.8e-32;
Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;
QY 1 NLVQFGVMIERMTGK-SALQYNDYGCYCGIGSHWPFVDQTDWCCHAHDCCVGRLEKLGCE 59
DB 1 NLVNFHRMIKLTGKKAALSFGYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 60
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYKHYHVPNKLCTGP 119
DB 61 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 120
QY 120 TPPC 123
DB 121 TPRC 124
RESULT 3
US-09-975-456B-6
; Sequence 6, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 2.1
; SEQ ID NO 6
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-6
Query Match 49.9%; Score 360.5; DB 10; Length 144;
Best Local Similarity 55.6%; Pred. No. 6.8e-32;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 1 NLVQFGVMIERMTGK-SALQYNDYGCYCGIGSHWPFVDQTDWCCHAHDCCVGRLEKLGCE 59
DB 21 NLVNFHRMIKLTGKKAALSFGYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 80
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYKHYHVPNKLCTGP 119
DB 61 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 140
US-10-205-823-325
; Sequence 325, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wansley, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 325
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-205-823-325
Query Match 49.9%; Score 360.5; DB 14; Length 144;
Best Local Similarity 55.6%; Pred. No. 6.8e-32;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;
QY 1 NLVQFGVMIERMTGK-SALQYNDYGCYCGIGSHWPFVDQTDWCCHAHDCCVGRLEKLGCE 59
DB 21 NLVNFHRMIKLTGKKAALSFGYCHGCGVGRGSPKDATDRCCVTHDCCYKRLKRGCG 80
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYKHYHVPNKLCTGP 119
DB 81 TKFLSYKFSNSKSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 140
QY 120 TPPC 123
DB 141 TPRC 144
RESULT 5
US-10-116-275-269
; Sequence 269, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elan Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
```



ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0403 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 984837  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-10-124-591-3  
Query Match 47.2%; Score 341; DB 13; Length 146;  
Best Local Similarity 52.8%; Pred. No. 9.9e-30;  
Matches 66; Conservative 9; Mismatches 48; Indels 2; Gaps 2;  
QY 1 NLVQGVMIKMTGKSA-LQYNDYCYGCGIGGSHWPVDQTDWCCHADCCVGRLEKLGCE 59  
DB 22 NIAQFGEIRUKTKRAELSAFYGCHGGLGGKSPKDATDRCCVTHDCCYKSLKSGCG 81  
QY 60 PKLEKYLFSVSRGIFCA-GRITTCQRLTCBCKRAALCFRRNLGTYNRYKHYAHYPNKLTCTG 118  
DB 82 TKLLKYKSHOGGQITCSANQNSCKRLCQCDKAAAEFCFARNKTKYSLKYQFYNNMFCCKG 141  
QY 119 PTPPC 123  
DB 142 KKPXC 146  
RESULT 9  
US-10-124-591-4  
Sequence 4, Application US/10124591  
Publication No. US20020177208A1  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
Bandman, Olga  
Guegler, Karl J.  
Shah, Purvi  
Corley, Neil C.  
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/124,591  
FILING DATE: 16-Apr-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/489,770  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/966,317  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0403 US  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 204319  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-124-591-4  
Query Match 46.7%; Score 337; DB 13; Length 146;  
Best Local Similarity 50.4%; Pred. No. 2.8e-29;  
Matches 63; Conservative 14; Mismatches 46; Indels 2; Gaps 2;  
QY 1 NLVQGVMIKMTGKSA-LQYNDYCYGCGIGGSHWPVDQTDWCCHADCCVGRLEKLGCE 59  
DB 22 SLLEFGQMLFKTKRADVSFYGCHGCGVGRGSPKDATDWCCTVTHDCCVNRLEKGGCG 81  
QY 60 PKLEKYLFSVSRGIFCA-GRITTCQRLTCBCKRAALCFRRNLGTYNRYKHYAHYPNKLTCTG 118  
DB 82 TKFLTYKFSYRGGQITSCSTNODSCRKQLCQCDKAAAEFCFARNKTKYSLKYQFYNNMFCCKG 141  
QY 119 PTPPC 123  
DB 142 KTPSC 146  
RESULT 10  
US-09-917-805-7  
Sequence 7, Application US/09917805  
Publication No. US2004007973A1  
GENERAL INFORMATION:  
APPLICANT: STYME, Sten  
APPLICANT: STAHL, Ulf  
APPLICANT: EK, Bo  
APPLICANT: SJODAHL, Staffan  
TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF  
FILE REFERENCE: STYME-1  
CURRENT APPLICATION NUMBER: US/09/917,805  
CURRENT FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 09/155,124  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: PCT/SE97/00554  
PRIOR FILING DATE: 1997-03-27  
PRIOR APPLICATION NUMBER: 9601237.2  
PRIOR FILING DATE: 1996-03-29  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 138  
TYPE: PPT  
ORGANISM: Bothrops jararacussu  
US-09-917-805-7  
Query Match 46.5%; Score 335.5; DB 12; Length 138;  
Best Local Similarity 50.0%; Pred. No. 3.8e-29;  
Matches 62; Conservative 12; Mismatches 47; Indels 3; Gaps 2;  
QY 1 NLVQGVMIKMTGKSA-LQYNDYCYGCGIGGSHWPVDQTDWCCHADCCVGRLEKLGCE 59  
DB 17 DLWQFGQMLFKTKRADVSFYGCHGCGVGRGSPKDATDRCCVTHDCCYKSLKSGCG 74  
QY 60 PKLEKYLFSVSRGIFCA-GRITTCQRLTCBCKRAALCFRRNLGTYNRYKHYAHYPNKLTCTG 119  
DB 75 PKTDRTYSYRENGVILICGEGTFCERQICECDKAAAEFCFARNLRTYKRYMAYPDVLCKKP 134  
QY 120 TTPC 123  
DB 135 AEKC 138

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RESULT 11
US-09-917-805-6
; Sequence 6, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYME, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SJODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: STYME=1
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 1999-03-02
; PRIOR FILING DATE: 1999-03-02
; PRIOR FILING DATE: 1997-03-27
; PRIOR FILING DATE: 1997-03-27
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Vipera ammodytes
US-09-917-805-6

Query Match      45.8%; Score 330.5; DB 12; Length 138;
Best Local Similarity 47.8%; Pred. No. 1.4e-28;
Matches 59; Conservative 18; Mismatches 44; Indels 3; Gaps 2;

QY      1 NLVQFGVMIEKMTGKSA-LQYNDYCYCGIGGSHWPVDQTDWCCCHAHDCCYGRLEKLGCE 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      17 SLLEFGMILGERGKPLTSYSYGYCGVGGTGPDKATDRCCFVHDCCYGNLP--DCS 74
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 PKLEKLFVSVERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYKHYAPNKLCTGP 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      75 PKTRKYHRENGAIVCGKGTSCENRICEDRAAALCFRRNLKTYNYIYRNIPDFLCKE 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      120 TPPC 123
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Db      135 SEKC 138

RESULT 12
US-09-917-805-2
; Sequence 2, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYME, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SJODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: STYME=1
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 1999-03-02
; PRIOR FILING DATE: 1997-03-27
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Trimeresurus flavoviridis
US-09-917-805-2
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Query Match      43.1%; Score 311.5; DB 12; Length 138;
Best Local Similarity 50.8%; Pred. No. 1.7e-26;
Matches 63; Conservative 12; Mismatches 44; Indels 5; Gaps 4;

QY      2 LVQFGVMIEKMTGKSA-LQYNDYCYCGIGGSHWPVDQTDWCCCHAHDCCYGRLEKLGCEP 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      18 LWQFENMIKVVKSGILSYSAICYCGWGGRGPKDADRCCFVHDCCYGKV--TGCNP 75
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 KLEKLFVSVERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR-KYAHYPNKLCTGP 119
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      76 KLGKTYSWNGDIVCEGEGPCKEV-CECDRAAALCFRDNLDTYDRNKYWYPASNCQED 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      120 TPPC 123
      :
Db      135 SEPC 138

RESULT 13
US-09-975-456B-2
; Sequence 2, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 2
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-2

Query Match      42.0%; Score 303; DB 10; Length 168;
Best Local Similarity 43.3%; Pred. No. 1.9e-25;
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;

QY      1 NLVQFGVMIEKMTGKSA-LQYNDYCYCGIGGSHWPVDQTDWCCCHAHDCCYGRLEKLGCE 59
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      21 SLNLKANVEAVTGESAILSFVGYGCGYGLGGRGQPKDEVDCCHAHDCCYQELFDQGC 80
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      60 PKLEKLFVS-SERGIFCA--GRITCQRLTCECDKRAALCFRRNLGTYNRYKHYAPNKL 116
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      81 PYVDHYDHTIENNTIEVCSDLNKTCECDKQTCWCDKNMVLCLMNQ--TYREYRGFLNVYC 138
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QY      117 TGPTPPC 123
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Db      139 QGPTPNC 145

RESULT 14
US-10-104-047-3735
; Sequence 3735, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR FILING DATE:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3735
; LENGTH: 168
; TYPE: PRT
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ORGANISM: Homo sapiens  
US-10-104-047-3735  
Query Match 42.0%; Score 303; DB 15; Length 168;  
Best Local Similarity 43.3%; Pred. No. 1.9e-25;  
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;  
QY 1 NLVQFGVMIEKMTGKSA-LQVNDYGCYCGIGGSHWPVDQTDWCHAHDCCYGRLEKLGCE 59  
DB 21 SLNLKAMVEAVTGRSAILSFVGYGCYGLGGRGQPKDEVDWCHAHDCCYQELFDGGCH 80  
QY 60 PKLEKYLFSV-SERGIFCA--GRTTQORLTCECDKRAALCFRRNLGTYNKRYAHYFNKLC 116  
DB 81 PYVDHYDHTIENNTIEIVCSDLNTECDKQTCMCDKNNVLCIMNQ--TYREYRGLNLYC 138  
QY 117 TGPTEPC 123  
DB 182 QGPTENC 188  
Search completed: July 3, 2004, 05:27:05  
Job time : 43.6302 secs

ORGANISM: Homo sapiens  
US-10-104-047-3735  
Query Match 42.0%; Score 303; DB 14; Length 211;  
Best Local Similarity 43.3%; Pred. No. 2.4e-25;  
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;  
QY 1 NLVQFGVMIEKMTGKSA-LQVNDYGCYCGIGGSHWPVDQTDWCHAHDCCYGRLEKLGCE 59  
DB 64 SLNLKAMVEAVTGRSAILSFVGYGCYGLGGRGQPKDEVDWCHAHDCCYQELFDGGCH 123  
QY 60 PKLEKYLFSV-SERGIFCA--GRTTQORLTCECDKRAALCFRRNLGTYNKRYAHYFNKLC 116  
DB 124 PYVDHYDHTIENNTIEIVCSDLNTECDKQTCMCDKNNVLCIMNQ--TYREYRGLNLYC 181  
RESULT 15  
US-10-345-680-23  
; Sequence 23, Application US/10345680  
; Publication No. US20030148394A1  
; GENERAL INFORMATION:  
; APPLICANT: Millennium Pharmaceuticals, Inc.  
; APPLICANT: Silos-Santiago, Inmaculada  
; APPLICANT: Venkateswarlu, Karicheti  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING  
; TITLE OF INVENTION: UROLOGICAL DISORDERS USING 1435, 559, 34021, 44099, 25278,  
; TITLE OF INVENTION: 641, 260, 55089, 21407, 42032, 46656, 62553, 302, 323,  
; TITLE OF INVENTION: 12303, 985, 12327, 13601, 18926, 318, 2058 OR 6351 MOLECULES.  
; FILE REFERENCE: MP102-012PIRNM.OMNI  
; CURRENT APPLICATION NUMBER: US/10/345,680  
; CURRENT FILING DATE: 2003-01-16  
; PRIOR APPLICATION NUMBER: US 60/349,511  
; PRIOR FILING DATE: 2002-01-18  
; PRIOR APPLICATION NUMBER: US 60/360,500  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/365,041  
; PRIOR FILING DATE: 2002-03-15  
; PRIOR APPLICATION NUMBER: US 60/374,063  
; PRIOR FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US 60/403,468  
; PRIOR FILING DATE: 2002-08-14  
; PRIOR APPLICATION NUMBER: US 60/414,262  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: US 60/419,986  
; PRIOR FILING DATE: 2002-10-21  
; PRIOR APPLICATION NUMBER: US 60/423,809  
; PRIOR FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/429,797  
; PRIOR FILING DATE: 2002-11-26  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 211  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-345-680-23

Query Match 42.0%; Score 303; DB 14; Length 211;  
Best Local Similarity 43.3%; Pred. No. 2.4e-25;  
Matches 55; Conservative 18; Mismatches 48; Indels 6; Gaps 4;  
QY 1 NLVQFGVMIEKMTGKSA-LQVNDYGCYCGIGGSHWPVDQTDWCHAHDCCYGRLEKLGCE 59  
DB 64 SLNLKAMVEAVTGRSAILSFVGYGCYGLGGRGQPKDEVDWCHAHDCCYQELFDGGCH 123  
QY 60 PKLEKYLFSV-SERGIFCA--GRTTQORLTCECDKRAALCFRRNLGTYNKRYAHYFNKLC 116  
DB 124 PYVDHYDHTIENNTIEIVCSDLNTECDKQTCMCDKNNVLCIMNQ--TYREYRGLNLYC 181



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:13:08 ; Search time 25.9925 Seconds  
(without alignments)  
1493.077 Million cell updates/sec

Title: US-10-088-092A-30\_COPY\_20\_142

Perfect score: 722

Sequence: 1 NLVDFGMIEKTSALQY.....YNRYAHYFNKLCTGTPPPC 123

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rviro:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	349	48.3	146	11	Q91Y34
2	333.5	46.2	138	13	Q7T1D5
3	325.5	45.1	138	13	Q805A3
4	323.5	44.8	138	13	Q8AXY1
5	322.5	44.8	138	13	Q805A2
6	315.5	43.7	138	13	Q7ZTA8
7	314.5	43.6	138	13	Q7ZTA6
8	313.5	43.4	138	13	Q7T1D1
9	312.5	43.3	138	13	Q7T1D4
10	312.5	43.3	138	13	Q7T1D3
11	312.5	43.3	138	13	Q7T1D2
12	310.5	43.0	138	13	Q800C1
13	309.5	42.9	138	13	Q800C2
14	309.5	42.9	138	13	Q7ZTA7
15	305.5	42.3	138	13	Q800C4
16	303	42.0	168	4	Q8N217

## ALIGNMENTS

### RESULT 1

Q91Y34  
ID Q91Y34 PRELIMINARY; PRT; 146 AA.  
AC Q91Y34;  
DT 01-DEC-2001 (TREMELrel. 19, Created)  
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)  
DE Platelet phospholipase A2 precursor (Fragment).  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=wislar; TISSUE=Blood;  
RA Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;  
RT "Cloning and sequence determination of rat platelet phospholipase A2  
from whole blood";  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF365363; AAK52061.1;  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.  
DR GO; GO:0001604; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR PRINTS; PR00389; PHEHLIPASEA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR SMART; SM00085; PA2C; 1.  
DR PROSITE; PS00119; PA2 ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
KW Signal.  
FT SIGNAL. 1 21  
FT CHAIN. 22 >146  
FT NON\_TER. 146 146  
SQ SEQUENCE 146 AA; 16306 MW; 60C1C9EC85DCBD67 CRC64;

POTENTIAL.  
PLATELET PHOSPHOLIPASE A2.

Query Match 48.3%; Score 349; DB 11; Length 146;  
Best Local Similarity 51.2%; Pred. No. 3.1e-33;  
Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

Q7T2R1 vipera russ  
Q800C3 crotalus vi  
Q8CE14 mus musculu  
Q8T3T5 vipera russ  
Q8N435 homo sapien  
Q7Z3Q1 vipera russ  
Q7T3S7 echis carin  
Q804D7 bothrops ja  
Q8K0Y1 mus musculu  
Q8J93 mus musculu  
Q7C1C6 vipera aspi  
Q8C5Y6 mus musculu  
Q9QX68 mesocricetu  
Q8AY48 bungarus ca  
Q8AXW0 bungarus mu  
Q8AXW1 bungarus mu  
Q7L1R0 bungarus fl  
Q7Z60 rana catesb  
Q8AXW2 bungarus mu  
Q7L1R1 bungarus fl  
Q9DEB0 pagrus majo  
Q8AXW7 micrurus co  
Q8XW8 adamsia car  
Q7C2Q4 bungarus fl  
Q80211 bungarus ca  
Q9U8P8 asterina pe  
Q7C2Q5 bungarus fl  
Q9YH62 dicentrarch  
Q9U8P9 asterina pe

QY 1 NLVQFGVMIEKMTGSA-LQNDYGCYGGIGSHWPVDQTDWCHADCCYGRLEKLGCE 59  
DB 22 SLLEFGQMIFPKTKRADVSYGFYGCYGGVGRGSPKQDADTDCVTHDCCYNLEKRGCG 81  
QY 60 PKLEKYLFSVSERGIFCA-GRITTCORLTCECDKRAALCFRRNLGTYNRKYAHYFNKLTG 118  
DB 82 TKFTYFVSRGHISCTWDSCKQLCCDRAAEFCFARNKKSYSLKVFYFNKFCG 141  
QY 119 TTPPC 123  
DB 142 KTPSC 146  
RESULT 2  
Q7TID5 PRELIMINARY; PRT; 138 AA.  
AC Q7TID5  
DT 01-OCT-2003 (TREMBlrel. 25, Created)  
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Phospholipase A2.  
GN PLA2VB.  
OS Vipera berus (Common viper).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Viperinae; Vipera.  
OX NCBI\_TaxID=31156;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=22707820; PubMed=12823540;  
RX Guillen L., Bouchier C., Garrigues T., Wisner A., Choumet V.;  
RT "Sequences and structural organization of phospholipase A2 genes from  
RT Vipera aspis aspis, V. aspis zinnikeri and Vipera berus berus venom.  
RT Identification of the origin of a new viper population based on  
RT amodycin II heterogeneity";  
RL Eur. J. Biochem. 270:2697-2706(2003).  
DR EMBL; AY158636; AAN59982.1; -.  
SQ SEQUENCE 138 AA; 15716 MW; 79B9F9E0D16C9CBB CRC64;  
Query Match 46.2%; Score 333.5; DB 13; Length 138;  
Best Local Similarity 48.4%; Pred. No. 2e-31;  
Matches 60; Conservative 14; Mismatches 47; Indels 3; Gaps 2;  
QY 1 NLVQFGVMIEKMTGSA-LQNDYGCYGGIGSHWPVDQTDWCHADCCYGRLEKLGCE 59  
DB 17 NLVQFGVMIEKMTGSA-LQNDYGCYGGIGSHWPVDQTDWCHADCCYGRLEKLGCE 74  
QY 60 PKLEKYLFSVSERGIFCA-GRITTCORLTCECDKRAALCFRRNLGTYNRKYAHYFNKLTG 119  
DB 75 PKLSTYSFONGNIVCGNKYGLHICEDRVAACEQKNMTYNNKYSSNCQEN 134  
QY 120 TTPC 123  
DB 135 SDKC 138  
RESULT 3  
Q805A3 PRELIMINARY; PRT; 138 AA.  
AC Q805A3  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Phospholipase A2.  
GN PLA-N.  
OS Trimeresurus flavoviridis (Habu).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Trimeresurus.  
OX NCBI\_TaxID=88087;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,  
RA Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;  
RT "Interisland mutation of a novel phospholipase A2 from Trimeresurus  
RT flavoviridis venom and evolution of crotalinae group II phospholipase  
RT A2.";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB102728; BAC56892.1; -.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; P:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR PRINTS; PR00389; PHEHLIPASEA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR SMART; SM00085; PA2C; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
SQ SEQUENCE 138 AA; 15817 MW; A2F7B5A23897ECCS CRC64;  
Query Match 45.1%; Score 325.5; DB 13; Length 138;  
Best Local Similarity 49.2%; Pred. No. 1.8e-30;  
Matches 61; Conservative 13; Mismatches 47; Indels 3; Gaps 2;  
QY 1 NLVQFGVMIEKMTGSA-LQNDYGCYGGIGSHWPVDQTDWCHADCCYGRLEKLGCE 59  
DB 17 NLVQFGVMIEKMTGSA-LQNDYGCYGGIGSHWPVDQTDWCHADCCYGRLEKLGCE 74  
QY 60 PKLEKYLFSVSERGIFCA-GRITTCORLTCECDKRAALCFRRNLGTYNRKYAHYFNKLTG 119  
DB 75 PKSDIYSYSWKTGVIICGEGTECEKQICECDRAAAGVCGNLTYYKKYMPDFLCTDP 134  
QY 120 TTPC 123  
DB 135 TEKC 138  
RESULT 4  
Q8AXY1 PRELIMINARY; PRT; 138 AA.  
AC Q8AXY1  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Hypotensive phospholipase A2.  
OS Bothrops jararacussu (Jararacussu).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Bothrops.  
OX NCBI\_TaxID=8726;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Venom gland;  
RX MEDLINE=22157211; PubMed=12167491;  
RA Andriao-Escarso S.H., Soares A.M., Fontes M.R., Fuly A.L.,  
RA Correa F.M., Rosa J.C., Greene L.J., Giglio J.R.;  
RT "Structural and functional characterization of an acidic platelet  
RT aggregation inhibitor and hypotensive phospholipase A(2) from Bothrops  
RT jararacussu snake venom.";  
RL Biochem. Pharmacol. 64:723-732(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Venom gland;  
RX Roberto P.G., Kashima S., Soares A.M., Astolfi-Filho S., Giglio J.R.,  
RA Franca S.C.;  
RT "Functional and Structural Analysis of Acidic and Basic Phospholipases  
RT A2 from Bothrops jararacussu Snake Venom.";  
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY145936; AAN37410.1; -.  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; P:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.

DR PRINTS; PR00389; PHPHILIPASEA2.  
DR PRODOM; PM000303; PhospholipaseA2; 1.  
DR SMART; SM00085; PA2C; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
SQ SEQUENCE 138 AA; 15456 MW; 513647907BFD0F4E CRC64;

Query March 44.8%; Score 323.5; DB 13; Length 138;  
Best Local Similarity 46.8%; Pred. No. 3e-30;  
Matches 58; Conservative 16; Mismatches 47; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKWTGKS-ALQYNDYGCYCGIGGSHWPVDQTDWCCHAHDCYGRLEKLGCE 59  
DB 17 SLAQFGKINYVMGESGLVQLSYGCGIGGGQGTDTDRCCFVHDCCKGV--TGCD 74  
QY 60 PLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYKHYPNKLTGTP 119  
DB 75 PKIDSITYSKNGDGVVCGDDPCKKQICECDRVATTCFRDNKDTYDIKYWFYGAKNCCQEK 134  
QY 120 TPPC 123  
DB 135 SEPC 138

RESULT 5  
Q805A2 PRELIMINARY; PRT; 138 AA.  
AC Q805A2;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE P1A-N(O).  
GN PLA2.  
OS Trimeresurus flavoviridis (Habu).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;  
OC Viperidae; Crotalidae; Trimeresurus.  
OX NCBI\_TaxID=88087;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chikawa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,  
RA Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ohno M.;  
RT "interisland mutation of a novel phospholipase A2 from Trimeresurus  
RT flavoviridis venom and evolution of crotalinae group II phospholipase  
RT A2.";  
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB102729; BACS6893.1; ..  
DR GO; GO:000509; F:calcium ion binding; IEA.  
DR GO; GO:000423; F:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR PRINTS; PR00389; PHPHILIPASEA2.  
DR PRODOM; PM000303; PhospholipaseA2; 1.  
DR SMART; SM00085; PA2C; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
SQ SEQUENCE 138 AA; 15803 MW; A2F103123897ECCS CRC64;

Query March 44.8%; Score 323.5; DB 13; Length 138;  
Best Local Similarity 49.2%; Pred. No. 3e-30;  
Matches 61; Conservative 12; Mismatches 48; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKWTGKSALQ-QYNDYGCYCGIGGSHWPVDQTDWCCHAHDCYGRLEKLGCE 59  
DB 17 NLLQFNKMKIMTKXGPPFTYSYGCYCGWGRGKPKDATDRCCFVHDCCKVL--TDCS 74  
QY 60 PLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLTGYNRYKHYPNKLTGTP 119  
DB 75 PKIDSITYSKNTGVITCGEGTEKEKQICECDRAAAVCFGQNLRTYKNKYFYPFLCTDP 134  
QY 120 TPPC 123

Qy	1	NLVQGVGMIEKRTG-KSALQNDYGVCGTGGSHWFDQDMCAHDCYGRLEKCE	59
Db	17	NLSQFGDMINKTGFISYIYCYCGMGKGKPLDADRCFVHDCYGRVK--GCD	74
Qy	60	PXLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLCTYNRKYAHFNKLTCTGP	119
Db	75	PKMGTYSYSFQNGDIVCGGDDPCLRAVCECDRAAICFGENMNTYDKKTYLMSLFDCKEE	134
Qy	120	TPPC 123	
Db	135	SEOC 138	

Query Match	43.3%;	Score 312.5;	DB 13;	Length 138;
Best Local Similarity	47.6%;	Pred. No. 6.1e-29;		

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RC STRAIN=B6h;
RX MEDLINE=22510024; PubMed=12623078;
RA Tsai I.-H., Wang Y.M., Chen Y.H., Tu A.T.;
RT "Geographic variations, cloning, and functional analyses of the venom
RL acidic phospholipases A(2) of Crotalus viridis viridis.";
RN Arch. Biochem. Biophys. 411:289-296(2003).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=B6h;
RA Tsai I.-H., Wang Y.-M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF403137; AAC93140.1; -
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
DR SQ SEQUENCE 138 AA; 15545 MW; 2FE3D8F8D79141EC CRC64;

Query Match 43.0%; Score 310.5; DB 13; Length 138;
Best Local Similarity 46.0%; Pred. No. le-28;
Matches 57; Conservative 14; Mismatches 50; Indels 3; Gaps 2

Qy 1 NLVQGVMIKWTGKSA-LQNVGYCYGGI GGSHWPVDQTMCCHADCCYGRLEKLGC 59
Db 17 SLVQFETILMTAGRSGLWTSAYCGICGWGHGLPQDA'DRCCFVHDCCYCK--ATDCN 74
Qy 60 PKLEYLFVSVERGI'FCAGRTTCORLCCECDKKAALCFERNLGTNYNRKYAHYENKLCITGP 119
Db 75 PTIVSYTVSKNGELICEDDDPCKRQCVRVAACFRNI'FSYNNNYKRFPAENCREE 134

Qy 120 TPCC 123
Db 135 PEPC 136

RESULT 13
Q800C2 Q800C2 PRELIMINARY; PRT; 138 AA.
ID AC Q800C2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phospholipase A2.
OS Crotalus viridis viridis (Prairie rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8742;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B6g;
RX MEDLINE=22510024; PubMed=12623078;
RA Tsai I.-H., Wang Y.M., Chen Y.H., Tu A.T.;
RT "Geographic variations, cloning, and functional analyses of the venom
RL acidic phospholipases A(2) of Crotalus viridis viridis.";
RN Arch. Biochem. Biophys. 411:289-296(2003).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=B6g;
RA Tsai I.-H., Wang Y.-M.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF403135; AAC93139.1; -
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:15:00 ; Search time 14.4679 Seconds  
(without alignments)  
506.699 Million cell updates/sec

Title: US-10-088-092A-30

Perfect score: 817

Sequence: 1 MKSPHLVFLCLLVALVTGN.....YNRKYAHYPNKLGTGTPPC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

\* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	368.5	45.1	144	1	US-08-186-895-10
2	368.5	45.1	144	2	US-08-888-497-37
3	368.5	45.1	144	4	US-09-362-230-37
4	368.5	45.1	144	5	PCT-US94-07926-37
5	360.5	44.1	124	1	US-08-170-360-4
6	360.5	44.1	124	2	US-08-888-497-39
7	360.5	44.1	124	4	US-09-362-230-39
8	360.5	44.1	124	4	US-09-740-569-2
9	360.5	44.1	124	5	PCT-US94-07926-39
10	360.5	44.1	124	2	US-08-888-497-35
11	360.5	44.1	146	4	US-09-362-230-35
12	360.5	44.1	146	5	PCT-US94-07926-35
13	350	42.8	146	3	US-08-966-317-3
14	350	42.8	146	4	US-09-489-770-3
15	349.5	42.8	146	3	US-08-966-317-4
16	349.5	42.8	146	4	US-09-489-770-4
17	348	42.6	125	2	US-08-888-497-42
18	348	42.6	125	4	US-09-362-230-42
19	348	42.6	125	5	PCT-US94-07926-42
20	321	39.3	125	1	US-08-170-360-5
21	317.5	38.9	138	2	US-08-888-497-32
22	317.5	38.9	138	4	US-09-362-230-32
23	317.5	38.9	138	5	PCT-US94-07926-32
24	314.5	38.5	137	2	US-08-888-497-30
25	314.5	38.5	137	4	US-09-362-230-30
26	314.5	38.5	137	5	PCT-US94-07926-30
27	299.5	36.7	118	2	US-08-888-497-40

28	299.5	36.7	118	4	US-09-097-094-5	Sequence 5, Appli
29	299.5	36.7	118	4	US-09-362-230-40	Sequence 40, Appl
30	299.5	36.7	118	5	PCT-US94-07926-40	Sequence 40, Appl
31	299.5	36.7	122	1	US-07-734-534A-1	Sequence 1, Appli
32	296.5	36.3	117	2	US-08-888-497-44	Sequence 44, Appl
33	296.5	36.3	117	4	US-09-362-230-44	Sequence 44, Appl
34	296.5	36.3	117	5	PCT-US94-07926-44	Sequence 44, Appl
35	295.5	36.2	158	2	US-08-888-497-22	Sequence 22, Appl
36	295.5	36.2	158	4	US-09-362-230-22	Sequence 22, Appl
37	295.5	36.2	158	5	PCT-US94-07926-22	Sequence 22, Appl
38	287.5	35.2	165	3	US-08-966-317-1	Sequence 1, Appli
39	287.5	35.2	165	4	US-09-489-770-1	Sequence 1, Appli
40	286	35.0	130	2	US-08-888-497-43	Sequence 43, Appl
41	286	35.0	130	4	US-09-362-230-43	Sequence 43, Appl
42	286	35.0	130	5	PCT-US94-07926-43	Sequence 43, Appl
43	244	29.9	118	3	US-09-090-602-4	Sequence 4, Appli
44	231.5	28.3	146	2	US-08-888-497-34	Sequence 34, Appl
45	231.5	28.3	146	4	US-09-362-230-34	Sequence 34, Appl

#### ALIGNMENTS

RESULT 1  
US-08-186-895-10  
; Sequence 10, Application US/08186895  
; Patent No. 5538885  
; GENERAL INFORMATION:  
; APPLICANT: Hollis, Melvyn  
; APPLICANT: Needham, Maurice R.C.  
; APPLICANT: Gooding, Clare  
; APPLICANT: Grosveld, Franklin G.  
; TITLE OF INVENTION: Expression Systems  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Cushman, Darby & Cushman  
; STREET: 1615 L Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: U.S.A.  
; ZIP: 20036-5601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/186,895  
; FILING DATE: 27-JAN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/046,383  
; FILING DATE: 09-APR-1993  
; APPLICATION NUMBER: US/07/810,414  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kokulis, Paul N.  
; REGISTRATION NUMBER: 16,773  
; REFERENCE/DOCKET NUMBER: PKW/3893/93802/MJW  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-861-3000  
; TELEFAX: 202-822-0944  
; TELEX: 6714627 CUSH  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 144 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-186-895-10

Query Match 45.1%; Score 368.5; DB 1; Length 144;  
Best Local Similarity 52.1%; Pred. No. 5.1e-32;  
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;





RESULT 4  
PCT-US94-07926-37  
; Sequence 37, Application PC/TUS9407926  
; GENERAL INFORMATION:  
; APPLICANT: Tishfield, Jeffrey J.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
; ADDRESSEE: Russell PA  
; STREET: 200 East Broward Boulevard  
; CITY: Fort Lauderdale  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 33301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07926  
; FILING DATE: 15-JUL-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/097,354  
; FILING DATE: 26-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Manso, Peter J.  
; REGISTRATION NUMBER: 32,264  
; REFERENCE/DOCKET NUMBER: IN21044-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 305-527-2498  
; TELEFAX: 305-764-4996  
; INFORMATION FOR SEQ ID NO: 37:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 144 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
PCT-US94-07926-37

Query Match 45.1%; Score 368.5; DB 5; Length 144;  
Best Local Similarity 52.1%; Pred. No. 5.1e-32;  
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

QY 12 LLVALVT-----GNLVQGVMIKMTGK-SALQYNDYGCYGGSHWPDQTDWCC 62  
Db 5 LLLAVIMIFGLLQAGHNLNFMHMKLTTCGKEALSFGYGCYGGVGRGSPKDATDRCC 64

QY 63 HAHDCCYGRLEKLGCSFKLEKLPFSVBERGIFCAGRTTCQRLTCECDKRAALCFRNLGT 122  
Db 65 VTHDCCYKLEKRGCGTKFLSYKFSNSGRITCAKQDSCRSQLCECDKAAATCFARNKTT 124

QY 123 YNRKYAHYPNKLCTGPTPPC 142  
Db 125 YNKYQYYSNKHCRGSTPRC 144

RESULT 5  
US-08-170-360-4  
; Sequence 4, Application US/08170360  
; Patent No. 5656602  
; GENERAL INFORMATION:  
; APPLICANT: Tseng, Albert P. S.  
; APPLICANT: Inglis, Adam

; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Figg Ernst & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/170,360  
; FILING DATE: 03-MAR-1994  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PCT/AU92/00333  
; FILING DATE: 06-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: AU PK 7058  
; FILING DATE: 04-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ernst, Barbara G.  
; REGISTRATION NUMBER: 30,377  
; REFERENCE/DOCKET NUMBER: 1871-104A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)783-6040  
; TELEFAX: (202)783-6031  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
US-08-170-360-4

Query Match 44.1%; Score 360.5; DB 1; Length 124;  
Best Local Similarity 55.6%; Pred. No. 3.1e-31;  
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY 20 NLVQGVMIKMTGK-SALQYNDYGCYGGSHWPDQTDWCCAHDCYGRLEKLGCE 78  
Db 1 NLVNFHMKLTTCGKEALSFGYGCYGGVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60

QY 79 PKLEKLPFSVBERGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNRYKAYHYPNKLCTGP 138  
Db 61 TKFLSYKFSNSGRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKYQYYSNKHCRGS 120

QY 139 TPPC 142  
Db 121 TPRC 124

RESULT 6  
US-08-888-497-39  
; Sequence 39, Application US/08888497  
; Patent No. 5972877  
; GENERAL INFORMATION:  
; APPLICANT: Tishfield, Jay A.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:







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/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/966,317
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0403 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 146 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 984837
/ US-08-966-317-3

Query Match 42.8%; Score 350; DB 3; Length 146;
Best Local Similarity 53.1%; Pred. No. 4.9e-30;
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYGGSHWPFVDTDWCCHAHDCCYGRLEKL 75
DB 19 VQGNIAQFGEMIRLKTGKRAELSYAFYCHGCLGGKSPDADTRCCVTHDCCYKSLKS 78

QY 76 GCEPKLEKYLFSVSRGIFC-AGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKL 134
DB 79 GCGTKLLKYKSHQGQITCSANQNSCQRLCQCDKAAAECPARNKKTYSLKQFYFNNMF 138

QY 135 CTGPTPPC 142
DB 139 CKGKKPKC 146

RESULT 14
US-09-489-770-3
/ Sequence 3, Application US/09489770
/ Patent No. 6393f01
/ GENERAL INFORMATION:
/ APPLICANT: Hawkins, Phillip R.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Shah, Purvi
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/966,317
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/489,770
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/966,317
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0403 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-855-0555
/ TELEFAX: 650-845-4166
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 146 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: GenBank
/ CLONE: 984837
/ US-09-489-770-3

Query Match 42.8%; Score 350; DB 4; Length 146;
Best Local Similarity 53.1%; Pred. No. 4.9e-30;
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYGGSHWPFVDTDWCCHAHDCCYGRLEKL 75
DB 19 VQGNIAQFGEMIRLKTGKRAELSYAFYCHGCLGGKSPDADTRCCVTHDCCYKSLKS 78

QY 76 GCEPKLEKYLFSVSRGIFC-AGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKL 134
DB 79 GCGTKLLKYKSHQGQITCSANQNSCQRLCQCDKAAAECPARNKKTYSLKQFYFNNMF 138

QY 135 CTGPTPPC 142
DB 139 CKGKKPKC 146

RESULT 15
US-08-966-317-4
/ Sequence 4, Application US/08966317
/ Patent No. 6103469
/ GENERAL INFORMATION:
/ APPLICANT: Hawkins, Phillip R.
/ APPLICANT: Bandman, Olga
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Shah, Purvi
/ APPLICANT: Corley, Neil C.
/ TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Dr.
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/966,317
/ FILING DATE: Filed Herewith
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:17:51 ; Search time 50.3698 Seconds  
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877.555 Million cell updates/sec

Title: US-10-088-092a-30

Perfect score: 817

Sequence: 1 MKSPHLVFLCLVALVTGN.....YNRKYAHYFNKLTGTPTPC 142

Scoring table: BLOSUM62

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Searched: 1276540 seqs, 311293816 residues

Total number of hits satisfying chosen parameters: 1276540

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications AA:  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	817	100.0	154	10	US-09-975-456B-8
2	370	45.3	164	9	US-09-925-300-1010
3	368.5	45.1	144	10	US-09-975-456B-6
4	368.5	45.1	144	14	US-10-205-823-325
5	368.5	45.1	144	15	US-10-116-275-269
6	360.5	44.1	124	14	US-10-255-576-2
7	350	42.8	146	9	US-09-993-999-8
8	350	42.8	146	13	US-10-124-591-3
9	349.5	42.8	138	12	US-09-917-805-7
10	349.5	42.8	146	13	US-10-124-591-4
11	349.5	42.3	138	12	US-09-917-805-6
12	325.5	39.8	138	12	US-09-917-805-2
13	317.5	38.9	138	10	US-09-975-456B-9
14	310.5	38.0	145	9	US-09-969-384-17
15	310.5	38.0	145	10	US-09-975-456B-7

16	309	37.8	168	10	US-09-975-456B-2
17	309	37.8	168	15	US-10-104-047-3735
18	309	37.8	211	14	US-10-345-680-23
19	309	37.8	211	15	US-10-295-027-195
20	309	37.8	211	16	US-10-275-998-2
21	309	37.8	211	16	US-10-188-832-80
22	308.5	37.8	145	9	US-09-835-996A-6
23	308.5	37.8	150	12	US-10-296-115-1342
24	306.5	37.5	137	9	US-09-993-999-9
25	299.5	36.7	118	9	US-09-987-655-5
26	299.5	36.7	118	9	US-09-987-675-5
27	287.5	35.2	135	10	US-09-975-456B-10
28	287.5	35.2	165	13	US-10-124-591-1
29	283.5	34.4	145	12	US-09-917-805-9
30	281	34.4	145	12	US-09-917-805-4
31	260	31.8	145	12	US-09-917-805-5
32	231.5	28.3	145	12	US-09-917-805-8
33	229.5	28.1	146	12	US-09-917-805-1
34	227.5	27.8	148	10	US-09-975-456B-5
35	227.5	27.8	148	12	US-09-917-805-3
36	227.5	27.8	156	9	US-09-925-297-511
37	225	27.5	146	9	US-09-993-999-7
38	210	25.7	151	12	US-10-398-663-7
39	203.5	24.9	152	14	US-10-230-058A-15
40	193.5	23.7	133	15	US-10-371-725-7
41	193	23.6	116	10	US-09-946-374-378
42	193	23.6	116	12	US-10-147-493-534
43	193	23.6	116	12	US-10-145-127-534
44	193	23.6	116	12	US-10-160-503-534
45	193	23.6	116	12	US-10-143-118-534

#### ALIGNMENTS

#### RESULT 1

US-09-975-456B-8  
; Sequence 8, Application US/09975456B  
; Publication No. US20030073087A1  
; GENERAL INFORMATION:  
; APPLICANT: LAZDUNSKI, MICHEL  
; APPLICANT: LAMBEAU, GERARD  
; APPLICANT: VALENTIN, EMMANUEL  
; TITLE OF INVENTION: NOVEL MANWALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2  
; FILE REFERENCE: 1478-R-00  
; CURRENT APPLICATION NUMBER: US/09/975,456B  
; PRIOR FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: 60/239,491  
; PRIOR FILING DATE: 2000-10-11  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 2.1  
; SEQ ID NO 8  
; LENGTH: 154  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-975-456B-8

Query Match	100.08	Score	817	DB	10	Length	154
Best Local Similarity	100.08	Pred. No.	8.9e-82	Mismatches	0	Indels	0
Matches	142	Conservative	0	Gaps	0		
Qy	1	MKSPHLVFLCLVALVTGNLVQFGVMIEKMTGKSALQYNDYGYCGIGGSHWPVDQTDW	60				
Db	13	MKSPHLVFLCLVALVTGNLVQFGVMIEKMTGKSALQYNDYGYCGIGGSHWPVDQTDW	72				
Qy	61	CCHAHDCCYGRLKLGCEPKLEKYLFSVSESGIFCAGRTTCQRLTCECDKKAALCFRRNL	120				
Db	73	CCHAHDCCYGRLKLGCEPKLEKYLFSVSESGIFCAGRTTCQRLTCECDKKAALCFRRNL	132				
Qy	121	GTYNKYAHYFNKLTGTPTPC	142				
Db	133	GTYNKYAHYFNKLTGTPTPC	154				





APPLICANT: Lambkin, Imelda  
APPLICANT: Higgins, Lisa  
TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and  
FILE REFERENCE: E1067/20087  
CURRENT FILING DATE: 2002-10-04  
NUMBER OF SEQ ID NOS: 349  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 269  
LENGTH: 144  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-116-275-269

Query Match 45.1%; Score 368.5; DB 15; Length 144;  
Best Local Similarity 52.1%; Pred. No. 1.8e-32;  
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;

QY 12 LLVALVT-----GNLVFGVMIEKMTGK-SALQNDYGCYGGSHWPVDQTDWCC 62  
DQ 5 LLLAVIMIFGLQAHGNLVNFRHMKLTGKEAALSYFGYCHGCGVGRGSPKDATDRCC 64  
QY 63 HAHDCYGRLEKLCCEPKLEKLFVSERGIKAGTTCQRLTCECDKRAALCFRNLGT 122  
DQ 65 VTHDCYRLEKRCGCTGKFLSYKFSNSGRITCAKQDSRSQLCECDKAAATCFARNKT 124  
QY 123 YNRKYAHYPNKLGTGPTTPC 142  
DQ 125 YNKYQYYSNKHCRGSTPRC 144

## RESULT 6

US-10-255-576-2  
Sequence 2, Application US/10255576  
Publication No. US20030161822A1  
GENERAL INFORMATION:  
APPLICANT: Weiss, Jerrold  
APPLICANT: Eisbach, Peter  
APPLICANT: Liang, Ning-Sheng  
TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE  
FILE REFERENCE: 5986/1E917US1  
CURRENT FILING DATE: 2002-09-25  
PRIORITY APPLICATION NUMBER: US/10/255,576  
PRIORITY FILING DATE: 2002-09-25  
PRIORITY FILING DATE: 2000-12-18  
PRIORITY FILING DATE: 2000-12-18  
PRIORITY FILING DATE: 1999-12-17  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 2  
LENGTH: 124  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-255-576-2

Query Match 44.1%; Score 360.5; DB 14; Length 124;  
Best Local Similarity 54.8%; Pred. No. 1.2e-31;  
Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;

QY 20 NLVQFGVMIEKMTGK-SALQNDYGCYGGSHWPVDQTDWCCCHADCCYGRLEKLCGE 78  
DQ 1 NLNVFRLILKLTGKEAALSYFGYCHGCGVGRGSPKDATDRCCVTHDCYKRLKRGCG 60  
QY 79 PKLEKLFVSERGIKAGTTCQRLTCECDKRAALCFRNLGTYNKYAHYPNKLCTGP 138  
DQ 61 TKFLSYKFSNSKRITCAKQDSRSQLCECDKAAATCFARNKTYNKYQYYSNKHCRGS 120  
QY 139 TTPC 142  
DQ 121 TTPC 124

## RESULT 7

US-09-993-999-8  
Sequence 8, Application US/09993999  
Patent No. US20020110891A1  
GENERAL INFORMATION:  
APPLICANT: HG, I-Cheng  
APPLICANT: Arm, Jonathan P.  
APPLICANT: Austen, K. Frank  
APPLICANT: Glincher, Laurie H.  
TITLE OF INVENTION: Phospholipase A2 Group Preferentially  
TITLE OF INVENTION: Expressed in Th2 Cells  
FILE REFERENCE: HUI-046  
CURRENT APPLICATION NUMBER: US/09/993,999  
CURRENT FILING DATE: 2001-11-06  
PRIORITY APPLICATION NUMBER: 60/246,316  
PRIORITY FILING DATE: 2000-11-06  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8  
LENGTH: 146  
TYPE: PRT  
ORGANISM: Mus musculus  
US-09-993-999-8

Query Match 42.8%; Score 350; DB 9; Length 146;  
Best Local Similarity 53.1%; Pred. No. 2e-30;  
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 17 VTGNLVQFGVMIEKMTGKSA-LQYNDYGCYGGSHWPVDQTDKCHADCCYGRLEKL 75  
DQ 19 VQGNIAQFGEMIRLKTGRAELSYAFYCHGCGVGRGSPKDATDRCCVTHDCYKSLKRS 78  
QY 76 GCEPKLEKLFVSERGIKAGTTCQRLTCECDKRAALCFRNLGTYNKYAHYPNKL 134  
DQ 79 GCGTLLKLYKSHQGGQITCSANQNSCQKRLCCQCDKAAAEFCFARNKTYSLKYQYFPMNF 138  
QY 135 CTGPTTPC 142  
DQ 139 CKGKPKC 146

## RESULT 8

US-10-124-591-3  
Sequence 3, Application US/10124591  
Publication No. US20020177208A1  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Bandman, Olga  
APPLICANT: Guegler, Karl J.  
APPLICANT: Shah, Purvi  
APPLICANT: Corley, Neil C.  
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESS: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/124,591  
FILING DATE: 16-Apr-2002  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: US/09/489,770  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/966,317  
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0403 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 984837  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

US-10-124-591-3

Query Match 42.8%; Score 350; DB 13; Length 146;  
Best Local Similarity 53.1%; Pred. No. 2e-30;  
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 17 VTGNLVQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHADCCYGRLEKL 75  
DB 19 VQNLIAQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHADCCYGRLEKL 78  
QY 76 GCEPKLEKLYFSVSRGIFC-AGSTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKL 134  
DB 79 CGGTKLLKYSHQGQITCSANQNSQKRLCQCDKAAACFARNKXTYSLKTYQFVPMF 138  
QY 135 CTGPTPPC 142  
DB 139 CKGKKPKC 146

## RESULT 9

US-09-917-805-7  
Sequence 7; Application US/09917805  
Publication No. US20040073973A1  
GENERAL INFORMATION:  
APPLICANT: STYME, Sten  
APPLICANT: STAHL, Ulf  
APPLICANT: EK, Bo  
APPLICANT: SJODAHL, Staffan  
TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF  
FILE REFERENCE: STYME-1  
CURRENT APPLICATION NUMBER: US/09/917,805  
CURRENT FILING DATE: 2001-07-31  
PRIOR APPLICATION NUMBER: 09/155,124  
PRIOR FILING DATE: 1999-03-02  
PRIOR APPLICATION NUMBER: PCT/SE97/00554  
PRIOR FILING DATE: 1997-03-27  
PRIOR APPLICATION NUMBER: 9601237.2  
PRIOR FILING DATE: 1996-03-29  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 138  
TYPE: PRT  
ORGANISM: Bothrops jararacussu

Query Match 42.8%; Score 349.5; DB 12; Length 138;  
Best Local Similarity 48.2%; Pred. No. 2.2e-30;  
Matches 66; Conservative 15; Mismatches 53; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLVQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAH 65  
DB 4 LWIMAVLLVGVGDDLWQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAH 63  
QY 66 DCCYGRLEKLEKLYFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125

DB 64 DCCYGLK--TNCKPKTDYRSYRENGVVICGEGTFCCKQICECDKAAAVCFRRNLRTYK 121  
QY 126 KYAHYPNKLCTGPTPPC 142  
DB 122 RYMAYPDVLCCKPAK 138

## RESULT 10

US-10-124-591-4  
Sequence 4; Application US/10124591  
Publication No. US20020177208A1  
GENERAL INFORMATION:  
APPLICANT: Hawkins, Phillip R.  
Bandman, Olga  
Guegler, Karl J.  
Shah, Purvi  
Corley, Neil C.  
TITLE OF INVENTION: HUMAN PHOSPHOLIPASE A2 PROTEIN  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/124,591  
FILING DATE: 16-Apr-2002  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/489,770  
FILING DATE: <Unknown>  
APPLICATION NUMBER: 08/966,317  
FILING DATE: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0403 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 146 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 204319  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 42.8%; Score 349.5; DB 13; Length 146;  
Best Local Similarity 47.2%; Pred. No. 2.3e-30;  
Matches 68; Conservative 18; Mismatches 51; Indels 7; Gaps 3;

QY 6 VLAVFLCLLVALVTGNLVQGVMIKMTGKSA-LQYNDYGCYCGIGGSHWPVDQTD 59  
DB 3 VILLAVVIMAFGSGTQVQGSLLFQGMILFKTGKADVSYGFYCHCGVGRGSPKDATD 62  
QY 60 WCHAHADCCYGRLEKLEKLYFSVSRGIFC-GRITTCQRLTCECDKRAALCFRR 118  
DB 63 WCVVTHDCCYNLEKRGCGTKELTYKFSYRGQISCTNQDSCKRQCCQCDKAAACEFAR 122  
QY 119 NLGTYNRYKHYAHYPNKLCTGPTPPC 142  
DB 123 NKKYSLSKYQFYLNKFKGKTPSC 146

```

RESULT 11
US-09-917-805-6
; Sequence 6, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYNE, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SJODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: STYNE=1
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 1996-03-29
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: PCT/SE97/00554
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: 9601237.2
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Viper a amodytes
US-09-917-805-6

Query Match      42.3%; Score 345.5; DB 12; Length 138;
Best Local Similarity 46.7%; Pred. No. 5.9e-30;
Matches 64; Conservative 21; Mismatches 47; Indels 5; Gaps 3;

QY 7 LVFLCLLVALVTGNLVQFGVMIEKMTGKSA-LQNDYCYCGIGGSHWPVDQTDWCCHAH 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 IVAVCLTG--VEGSLLEFGNMILGETGKNPLTSFYCYCGVGKGTPKDATDRCCFVH 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 66 DCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 DCCYGNLP--DCSPKTDTRYHRENGAIVCGKGTSCENRICECDRAAALCFRRNLGTYN 121
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 126 KYAHYPNKLCTGTPPC 142
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 122 IYRNPDLCKESEKC 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
US-09-917-805-2
; Sequence 2, Application US/09917805
; Publication No. US20040073973A1
; GENERAL INFORMATION:
; APPLICANT: STYNE, Sten
; APPLICANT: STAHL, Ulf
; APPLICANT: EK, Bo
; APPLICANT: SJODAHL, Staffan
; TITLE OF INVENTION: PLANT ENZYME AND USE THEREOF
; FILE REFERENCE: STYNE=1
; CURRENT APPLICATION NUMBER: US/09/917,805
; CURRENT FILING DATE: 2001-07-31
; PRIOR FILING DATE: 1999-03-02
; PRIOR FILING DATE: 1997-03-27
; PRIOR APPLICATION NUMBER: PCT/SE97/00554
; PRIOR FILING DATE: 1996-03-29
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Trimeresurus flavoviridis
US-09-917-805-2
```

```

Query Match      39.8%; Score 325.5; DB 12; Length 138;
Best Local Similarity 48.6%; Pred. No. 9.4e-28;
Matches 67; Conservative 15; Mismatches 51; Indels 5; Gaps 4;

QY 7 LVFLCLLVALVTGNLVQFGVMIEKMTGKSA-LQNDYCYCGIGGSHWPVDQTDWCCHAH 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 4 LWIMAVLLVGDGGLWQFENMIIVYKKSGLISYAYCYCGWGGRGPKDATDRCCFVH 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 66 DCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNR 125
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 DCCYGV--TGCNPKLGKTYTSWNGDIVCGDGPCKEV-CECDRAAALCFRRNLDTYDR 120
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 126 KYAHYPNKLCTGTPPC 142
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 NKWRYPASNCQEDSEPC 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-09-975-456B-9
; Sequence 9, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERAED
; APPLICANT: VALENTIN, EMMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 9
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-9

Query Match      38.9%; Score 317.5; DB 10; Length 138;
Best Local Similarity 45.7%; Pred. No. 7.1e-27;
Matches 59; Conservative 17; Mismatches 52; Indels 1; Gaps 1;

QY 9 FLCLLVALVTGNLVQFGVMIEKMTGKSA-LQNDYCYCGIGGSHWPVDQTDWCCHADC 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 10 FLACSVPAVQGLLDLKSIMIEKVTGNALTYGFCYCGWGGRTPKDGTDMCCWAHDH 69
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 68 CYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRY 127
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 70 CYGRLEKGCNIRTQSYKYRFAGVVTCPPGPFCHVNLCACDRLVYCLKRNLSYNPOY 129
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 128 AHYPNKLCT 136
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 130 QYFPNILCS 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 14
US-09-969-384-17
; Sequence 17, Application US/09969384
; Publication No. US20020192749A1
; GENERAL INFORMATION:
; APPLICANT: Moore, et al.
; TITLE OF INVENTION: Human Gene Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT055P1
; CURRENT APPLICATION NUMBER: US/09/969,384
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: PCT/US01/10542
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/236,384
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/194,118
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 27
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-969-384-17

Query Match      38.0%; Score 310.5; DB 9; Length 145;
Best Local Similarity 39.2%; Pred. No. 4.5e-26;
Matches 56; Conservative 23; Mismatches 57; Indels 7; Gaps 3;

Qy 7 LVFLCLLVAL-----VTGNLVQGVMIKMTGK-SALQYNDYCYCGIGGSHWPDQTDW 60
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 3 LALLCGLVWVWAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCCHGLGGRGQPKDATDW 62
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 CCHAHDCCYGRLKLEKPEKLYLFSVSRGIFCAGR-TTCORLTCECDKRAALCFRRN 119
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 63 CCQTHDCCYDHLKTQGGSIYKDYRYNFSQGNHCSDKGSWCEQQLCACDKEVAFCLKRN 122
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 120 LGTYNRKYAHYPNKLCTGTPPC 142
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 123 LDYQKRLRFYWRPHCRGQTPGC 145
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

RESULT 15
US-09-975-456B-7
; Sequence 7, Application US/09975456B
; Publication No. US20030073087A1
; GENERAL INFORMATION:
; APPLICANT: LAZDUNSKI, MICHEL
; APPLICANT: LAMBEAU, GERARD
; APPLICANT: VALENTIN, EMANUEL
; TITLE OF INVENTION: NOVEL MAMMALIAN SECRETED GROUP IIF PHOSPHOLIPASE A2
; FILE REFERENCE: 1478-R-00
; CURRENT APPLICATION NUMBER: US/09/975,456B
; CURRENT FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: 60/239,491
; PRIOR FILING DATE: 2000-10-11
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 2.1
; SEQ ID NO 7
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-975-456B-7

Query Match      38.0%; Score 310.5; DB 10; Length 145;
Best Local Similarity 39.2%; Pred. No. 4.5e-26;
Matches 56; Conservative 23; Mismatches 57; Indels 7; Gaps 3;

Qy 7 LVFLCLLVAL-----VTGNLVQGVMIKMTGK-SALQYNDYCYCGIGGSHWPDQTDW 60
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 3 LALLCGLVWVWAGVPIQGGILNLNKMVKQVTGKMPILSYWPYGCCHGLGGRGQPKDATDW 62
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 61 CCHAHDCCYGRLKLEKPEKLYLFSVSRGIFCAGR-TTCORLTCECDKRAALCFRRN 119
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 63 CCQTHDCCYDHLKTQGGSIYKDYRYNFSQGNHCSDKGSWCEQQLCACDKEVAFCLKRN 122
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 120 LGTYNRKYAHYPNKLCTGTPPC 142
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |
Qy 123 LDYQKRLRFYWRPHCRGQTPGC 145
Db | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | |

Search completed: July 3, 2004, 05:27:05
Job time : 52.3698 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2004, 05:12:38 ; Search time 10.1811 Seconds  
(without alignments)  
726.242 Million cell updates/sec

Title: US-10-088-092A-30

Perfect score: 817

Sequence: 1 MKSPHVLVFLCLLVALVTGN.....YNRKYAHYPNKLCTGTPPC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	817	100.0	142	1	PA2E_HUMAN
2	709	86.8	142	1	PA2E_MOUSE
3	373	45.7	137	1	PA2M_VIPAA
4	372	45.5	121	1	PA21_ERIMA
5	368.5	45.1	144	1	PA2A_HUMAN
6	359.5	44.0	146	1	PA2A_RAT
7	358.5	43.9	120	1	PA2Y_CERCE
8	358.5	43.9	138	1	PA2Q_TRIFL
9	355.5	43.5	138	1	PA2D_DABRR
10	355	43.5	121	1	PA2B_VIPAA
11	354	43.3	137	1	PA2B_VIPAA
12	351.5	43.0	138	1	PA2B_VIPAA
13	351.5	43.0	138	1	PA2M_TRIFL
14	350	42.8	123	1	PA21_AKPI
15	350	42.8	146	1	PA2A_MOUSE
16	349.5	42.8	138	1	PA21_BOTJR
17	348.5	42.7	138	1	PA26_TRIGA
18	348.5	42.7	138	1	PA2B_VIPAA
19	345.5	42.3	138	1	PA2A_VIPAA
20	345.5	42.3	138	1	PA2C_VIPAA
21	341.5	41.8	138	1	PA2A_TRIFL
22	340.5	41.7	122	1	PA2A_TRIFL
23	340	41.6	122	1	PA2A_BITCA
24	339.5	41.6	122	1	PA2X_TRIFL
25	339.5	41.6	138	1	PA2P_TRIFL
26	338.5	41.4	122	1	PA2B_AKHP
27	338.5	41.4	122	1	PA2B_TRIFL
28	338.5	41.4	138	1	PA2A_TRIFL
29	338.5	41.4	138	1	PA2A_TRIFL
30	336	41.1	145	1	PA2M_CAVPO
31	333.5	40.8	138	1	PA21_TRIGA
32	333.5	40.8	138	1	PA25_ECHOC
33	332.5	40.7	121	1	PA2B_DABRR

RESULT 1  
PA2E\_HUMAN  
ID PA2E\_HUMAN STANDARD; PRT; 142 AA.  
AC Q9NZK7;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)  
DE (Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE sPLA2) (sPLA(2)-IIE).  
GN PLA2G2E.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RX MEDLINE=2014788; PubMed=10681567;  
RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,  
FUJII N., Kawamoto K., Hanasaki K.;  
RT "Structures, enzymatic properties, and expression of novel human and  
mouse secretory phospholipase A(2)s";  
RL J. Biol. Chem. 275:5785-5793(2000).  
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. Has a preference for arachidonic-containing phospholipids.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and placenta.  
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.

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EMBL; AF189279; AAF36541.1; --  
RSP; P14555; IPOD.  
DR GO; GO:0004624; F:secreted phospholipase A2 activity; TAS.  
DR GO; GO:0005954; P:inflammatory response; TAS.  
DR GO; GO:0006644; P:phospholipid metabolism; TAS.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; Phoslip; 1  
DR PRINTS; PR00389; PHPLIPASEA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR SMART; SMO0085; PA2C; 1.  
DR PROSITE; PS00119; PA2 ASP; FALSE\_NEG.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
KW Hydrolase; Lipid degradation; Signal; Calcium.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.

34 332.5 40.7 122 1 PA22\_AKHA  
35 332.5 40.7 122 1 PA2\_VIPBB  
36 332.5 40.7 138 1 PA2A\_CROSS  
37 329.5 40.3 122 1 PA2D\_TRIGA  
38 329 40.3 144 1 PA2D\_MOUSE  
39 328.5 40.2 122 1 PA21\_AKHA  
40 328 40.1 139 1 PA2E\_AKHP  
41 326.5 40.0 138 1 PA21\_ECHOC  
42 325.5 39.8 121 1 PA22\_BRIMA  
43 325.5 39.8 122 1 PA28\_AKHP  
44 325.5 39.8 138 1 PA21\_TRIFL  
45 324.5 39.7 122 1 PA23\_TRIGA

#### ALIGNMENTS

FT ACT SITE 65 BY SIMILARITY.  
 FT ACT SITE 109 BY SIMILARITY.  
 FT DISULFID 44 135 BY SIMILARITY.  
 FT DISULFID 46 62 BY SIMILARITY.  
 FT DISULFID 61 115 BY SIMILARITY.  
 FT DISULFID 67 142 BY SIMILARITY.  
 FT DISULFID 68 108 BY SIMILARITY.  
 FT DISULFID 77 101 BY SIMILARITY.  
 FT DISULFID 95 106 BY SIMILARITY.  
 FT METAL 45 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL 47 (BY SIMILARITY).  
 FT METAL 47 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL 49 (BY SIMILARITY).  
 FT METAL 49 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL 66 (BY SIMILARITY).  
 FT METAL 66 CALCIUM (BY SIMILARITY).  
 SQ SEQUENCE 142 AA; 15989 MW; 30360EA710E141FB CRC64;  
 Query Match 100.0%; Score 817; DB 1; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 1e-79;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKSPHVLVFLCLLVLTGNLVQFGVMTKGSALQYNDYGCYGGGSHWPDQTDW 60  
 DB 1 MKSPHVLVFLCLLVLTGNLVQFGVMTKGSALQYNDYGCYGGGSHWPDQTDW 60  
 QY 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNL 120  
 DB 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNL 120  
 QY 121 GTYNKYAHYPNKLCTGTPPC 142  
 DB 121 GTYNKYAHYPNKLCTGTPPC 142  
 RESULT 2  
 ID PA2E\_MOUSE STANDARD; PRT; 142 AA.  
 AC Q9QUL3;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)  
 DE (Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE sPLA2) (sPLA2(2)-IIE).  
 GN PLA2G2E.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=2002639; PubMed=10531313;  
 RA Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;  
 RT "On the diversity of secreted phospholipases A2. Cloning, tissue  
 RT distribution, and functional expression of two novel mouse group II  
 RT enzymes."  
 RL J. Biol. Chem. 274:31195-31202(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
 RC STRAIN=BALE/GI;  
 RX MEDLINE=20148786; PubMed=10681567;  
 RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,  
 RA Fujii N., Kawamoto K., Hanasaki K.;  
 RT "Structures, enzymatic properties, and expression of novel human and  
 RT mouse secretory phospholipase A(2)s."  
 RL J. Biol. Chem. 275:5785-5793(2000).  
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
 CC acyl groups in 3-sn-phosphoglycerides.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 CC acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Highly expressed in uterus, and at lower  
 CC levels in various other tissues.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
 CC -----  
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 CC or send an email to license@isb-sib.ch).  
 CC -----  
 CC EMBL; AF166098; AAF04499.1; -;  
 CC EMBL; AF12984; AAF22290.1; -;  
 CC HSSP; P14555; IPOD.  
 CC MGD; MGI:1349660; Pla2g2e.  
 CC InterPro; IPR001211; PhospholipaseA2.  
 CC Pfam; PF00068; phoslip; 1.  
 CC PRINTS; PR00389; PHPLIPASEA2.  
 CC ProDom; PD000303; PhospholipaseA2; 1.  
 CC SMART; SM00085; PA2c; 1.  
 CC PROSITE; PS00119; PA2\_ASP; FALSE\_NEG.  
 CC PROSITE; PS00118; PA2\_HIS; 1.  
 CC Hydrolase; Lipid degradation; Signal; Calcium.  
 KW SIGNAL 1 19  
 FT CHAIN 20 142  
 FT ACT\_SITE 65 65  
 FT ACT\_SITE 109 109  
 FT DISULFID 44 135  
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 FT DISULFID 68 108  
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 FT DISULFID 95 106  
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 QY 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNL 120  
 DB 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNL 120  
 QY 121 GTYNKYAHYPNKLCTGTPPC 142  
 DB 121 GTYNKYAHYPNKLCTGTPPC 142  
 RESULT 3  
 ID PA2N\_VIPAA STANDARD; PRT; 137 AA.  
 AC P34180; Q91967;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 16-FEB-1994 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Phospholipase A2, neutral precursor (EC 3.1.1.4) (Ammodytin I2)  
 DE (Phosphatidylcholine 2-acylhydrolase).  
 GN AMI2.  
 OS Vipera ammodytes ammodytes (Western sand viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;



Query Match 45.5%; Score 372; DB 1; Length 121;  
 Best Local Similarity 56.5%; Pred. No. 1.5e-32;  
 Matches 70; Conservative 8; Mismatches 42; Indels 4; Gaps 3;

QY 20 NLVFGVMIKMTGKSA-LQYNDVGCYCGIGSHFVDQDWCCHADCCYGRLEKLGCE 78  
 DB 1 NLYDFGKMFMTGKSAALLSYDGYCGWGGKGPLDTRCCFVHDCYGRVN--GCN 58

QY 79 PKLEKLYFVSERGIIFCAGRTTCORLTCECDKRAALCFRNLGTYNRYKAYHYNKLTGTP 138  
 DB 59 PKLSTYSYFQNGDIVCGDDNACLRVCEORVAACIFGKNTYDKYDYSSQCT-E 117

QY 139 TPPC 142  
 DB 118 TEQC 121

RESULT 5  
 FA2A HUMAN STANDARD; PRT; 144 AA.

AC P14555; Q3UCD2;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)  
 DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)  
 DE (GLIC sPLA2) (Non-pancreatic secretory phospholipase A2) (NPS-PLA2).  
 GN PLA2G2A OR PLA2B OR RASFA OR PLA2L.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Rheumatoid arthritic synovial fluid;  
 RX MEDLINE=89174566; PubMed=2925608;  
 RA Seilhamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,  
 RA Kless J., Johnson L.K.;  
 RT "Cloning and recombinant expression of phospholipase A2 present in  
 RT rheumatoid arthritic synovial fluid.";  
 RL J. Biol. Chem. 264:5335-5338(1989).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=89174633; PubMed=2925633;  
 RA Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,  
 RA Tizard R., Pepinsky R.B.;  
 RT "Structure and properties of a human non-pancreatic phospholipase  
 RT A2.";  
 RL J. Biol. Chem. 264:5768-5775(1989).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=91050834; PubMed=2239446;  
 RA Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;  
 RT "Structure and properties of a secreted phospholipase A2 from human  
 RT platelets.";  
 RL Adv. Exp. Med. Biol. 275:35-53(1990).  
 RN [4]

RP SEQUENCE FROM N.A.  
 RC TISSUE=Prostate;  
 RX MEDLINE=2238257; PubMed=1247793;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]

RP SEQUENCE OF 21-144.  
 RC TISSUE=Spleen;  
 RX MEDLINE=89374261; PubMed=2775276;  
 RA Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;  
 RT "The primary structure of a membrane-associated phospholipase A2 from  
 RT human spleen.";  
 RL Biochem. Biophys. Res. Commun. 163:42-48(1989).  
 RN [6]

RP SEQUENCE OF 21-54.  
 RC TISSUE=Synovial fluid;  
 RX MEDLINE=89197814; PubMed=3240982;  
 RA Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;  
 RT "Amino acid composition and NH2-terminal amino acid sequence of human  
 RT phospholipase A2 purified from rheumatoid synovial fluid.";  
 RL J. Biochem. 104:326-328(1988).  
 RN [7]

RP SEQUENCE OF 21-33.  
 RC TISSUE=Synovial fluid;  
 RX MEDLINE=89076274; PubMed=3202859;  
 RA Lai C.Y., Wada K.;  
 RT "Phospholipase A2 from human synovial fluid: purification and  
 RT structural homology to the placental enzyme.";  
 RL Biochem. Biophys. Res. Commun. 157:488-493(1988).  
 RN [8]

RP SEQUENCE OF 21-75.  
 RC TISSUE=ileal mucosa;  
 RX MEDLINE=94002200; PubMed=8399335;  
 RA Minami T., Tojo H., Shinomura Y., Matsuzawa Y., Okamoto M.;  
 RT "Purification and characterization of a phospholipase A2 from human  
 RT ileal mucosa.";  
 RL Biochim. Biophys. Acta 1170:125-130(1993).  
 RN [9]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=91287826; PubMed=2062381;  
 RA Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,  
 RA Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,  
 RA Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,  
 RA Warrick M.W., Jones N.D.;  
 RT "Structure of recombinant human rheumatoid arthritic synovial fluid  
 RT phospholipase A2 at 2.2-A resolution.";  
 RL Nature 352:79-82(1991).  
 RN [10]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=92054586; PubMed=1948070;  
 RA Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,  
 RA Sigler P.B.;  
 RT "Structures of free and inhibited human secretory phospholipase A2  
 RT from inflammatory exudate.";  
 RL Science 254:1007-1010(1991).  
 RN [11]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=95393225; PubMed=7664108;  
 RA Schevitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,  
 RA Dillard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihelich E.D.,  
 RA Oikowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;  
 RT "Structure-based design of the first potent and selective inhibitor  
 RT of human non-pancreatic secretory phospholipase A2.";  
 RL Nat. Struct. Biol. 2:458-465(1995).  
 RN [12]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=98207049; PubMed=9538252;  
 RA Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;  
 RT "Crystal structure of human secretory phospholipase A2-IIA complex  
 RT with the potent indolizine inhibitor 120-1032.";





RX MEDLINE=8818690; PubMed=3356705;  
 RA Ono T, Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.;  
 RT "Purification and characterization of a membrane-associated  
 phospholipase A2 from rat spleen. Its comparison with a cytosolic  
 phospholipase A2 S-1.";  
 RL J. Biol. Chem. 263:5732-5738(1988).  
 RN [7]  
 RP SEQUENCE OF 22-46.  
 RC TISSUE=Platelet;  
 RX MEDLINE=8800747; PubMed=3654593;  
 RA Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.;  
 RT "Amino acid composition and NH2-terminal amino acid sequence of rat  
 platelet secretory phospholipase A2.";  
 RL J. Biochem. 101:1311-1314(1987).  
 RN [8]  
 RP SEQUENCE OF 22-45.  
 RC TISSUE=Liver;  
 RX MEDLINE=8925484; PubMed=2722857;  
 RA Aarsman A.J., de Jong J.G.N., Arnoldussen E., Neys F.W.,  
 van Wassenar P.D., van den Bosch H.;  
 RT "Immunocaffinity purification, partial sequence, and subcellular  
 localization of rat liver phospholipase A2.";  
 RL J. Biol. Chem. 264:10008-10014(1989).  
 CC -!- FUNCTION: Thought to participate in the regulation of the  
 phospholipid metabolism in biomembranes including eicosanoid  
 biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-  
 acyl groups in 3-sn-phosphoglycerides.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1' calcium ion per subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.  
 CC -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells  
 and also extracellularly. The membrane-bound and secreted forms  
 are identical and are encoded by a single gene.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; D00523; BAA00410.1; -;  
 DR EMBL; M37127; AAA41223.1; -;  
 DR EMBL; M25148; AAA41920.1; -;  
 DR EMBL; X51529; CAA35909.1; -;  
 DR PIR; A33394; A33394.  
 DR HSP; P14555; IPOD.  
 DR InterPro: IPR001211; PhospholipaseA2.  
 DR Pfam; PF00068; phoslip; 1.  
 DR PRINTS; PR00389; PHPLIPASEA2.  
 DR ProDom; PD000303; PhospholipaseA2; 1.  
 DR SMART; SM00085; PA2c; 1.  
 DR PROSITE; PS00118; PA2\_HIS; 1.  
 DR PROSITE; PS00119; PA2\_ASP; 1.  
 KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium.  
 FT SIGNAL 1 21  
 FT CHAIN 22 146 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.  
 FT ACT\_SITE 68 68 BY SIMILARITY.  
 FT ACT\_SITE 113 113 BY SIMILARITY.  
 FT DISULFID 47 139 BY SIMILARITY.  
 FT DISULFID 49 65 BY SIMILARITY.  
 FT DISULFID 64 119 BY SIMILARITY.  
 FT DISULFID 70 146 BY SIMILARITY.  
 FT DISULFID 71 112 BY SIMILARITY.  
 FT DISULFID 80 105 BY SIMILARITY.  
 FT DISULFID 98 110 BY SIMILARITY.  
 FT METAL 48 48 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL 50 50 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL (BY SIMILARITY).

FT METAL 52 52 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL (BY SIMILARITY).  
 FT METAL 69 69 CALCIUM (BY SIMILARITY).  
 FT VARIANT 135 135 P -> L (POLYMORPHISM).  
 FT CONFLICT 22 22 S -> D (IN REF. 8).  
 FT CONFLICT 63 63 W -> E (IN REF. 5).  
 FT CONFLICT 69 69 D -> E (IN REF. 5).  
 FT CONFLICT 78 78 R -> S (IN REF. 5).  
 FT CONFLICT 85 85 L -> V (IN REF. 3).  
 FT CONFLICT 121 121 A -> S (IN REF. 5).  
 SQ SEQUENCE 146 AA; 16294 MW; 60DDC9E79BF109F7 CRC64;  
 Query Match 44.0%; Score 359.5; DB 1; Length 146;  
 Best Local Similarity 47.9%; Pred. No. 4e-31; Indels 7; Gaps 3;  
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 QY 6 VLVLCLLVAL-----VTGNLVQFGVMIEKMTGKSA-LQYNDYCYCGIGSHWPVQTD 59  
 DB 3 VLLLLAVVIMAFGSIQVQGSLLFQGMILFKTKRADVSYGFYGCYGVGGRGSPKDATD 62  
 QY 60 WCCHAHDCYGRLEKLGCEPKLEKYLFSVSRGIFCA-GRITCORLTCECDKRALCFRR 118  
 DB 63 WCVVTHDCYNRLEKRGCGGTRFLTYKFSYRGQISCSNTQDSCKRQLCCDKAAAECAF 122  
 QY 119 NLGTYNRYAHYPNKLCTGTPPC 142  
 DB 123 NKXSLKXQFYPNFKCKGKTPSC 146  
 RESULT 7  
 PA2 CERCE STANDARD; PRT; 120 AA.  
 ID PA2 CERCE  
 AC P21789;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).  
 OS Cerastes cerastes (Horned viper).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroides;  
 CC Viperidae; Viperinae; Cerastes.  
 CC NCBI\_TaxID=8697;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Baluchistan; TISSUE=Venom;  
 RX MEDLINE=91130587; PubMed=1993470;  
 RA Siddiqi A.R., Shafqat J., Zaidi Z.H., Joernvall H.;  
 RT "Characterization of phospholipase A2 from the venom of Horned viper  
 (Cerastes cerastes).";  
 RL FEBS Lett. 278:14-16(1991).  
 RN [2]  
 RP SEQUENCE OF 1-31.  
 RC STRAIN=Tunisia; TISSUE=Venom;  
 RX MEDLINE=90385487; PubMed=2402760;  
 RA Djebbari F.L., Martin-Eauclaire M.-F.;  
 RT "Purification and characterization of a phospholipase A2 from  
 Cerastes cerastes (horn viper) snake venom.";  
 RL Toxicon 28:637-646(1990).  
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
 acyl groups in 3-sn-phosphoglycerides.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1' calcium ion per subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MISCELLANEOUS: Strains variations are extensive for this enzyme.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II  
 subfamily.  
 CC PIR; A35950; A35950.  
 DR PIR; S13019; S13019.  
 DR HSP; P81458; LVIP.  
 DR InterPro: IPR001211; PhospholipaseA2.  
 DR Pfam; PF00068; phoslip; 1.  
 DR PRINTS; PR00389; PHPLIPASEA2.

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DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolyase; Lipid degradation; Calcium.
FT ACT_SITE 47 47 BY SIMILARITY.
FT ACT_SITE 89 89 BY SIMILARITY.
FT DISULFID 26 115 BY SIMILARITY.
FT DISULFID 28 44 BY SIMILARITY.
FT DISULFID 43 95 BY SIMILARITY.
FT DISULFID 50 88 BY SIMILARITY.
FT DISULFID 57 81 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 29 29 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 48 48 CALCIUM (BY SIMILARITY).
FT VARIANT 10 12 FKM -> KHK (IN STRAIN TUNISIA).
FT VARIANT 17 19 PIF -> ALL (IN STRAIN TUNISIA).
FT VARIANT 22 23 GD -> SA (IN STRAIN TUNISIA).
SQ SEQUENCE 120 AA; E5581FA7001C62C3 CRC64;

Query Match 43.9%; Score 358.5; DB 1; Length 120;
Best Local Similarity 54.2%; Pred. No. 4.2e-31;
Matches 64; Conservative 10; Mismatches 41; Indels 3; Gaps 2;

QY 20 NLVQFGVMIKMTGKSGAL-QYNDYGVCGYGGSHWPDQTDWCCHADCCYGRLEKLGCE 78
DB 1 NLVQFGVMIKMTGKSPFISYGYGVCGYGGGKTPTVDATDRCCFVHDCCYGRVN--SCN 58
QY 79 PLEKYLFSVSRGIFCAGETTCQRLTCECDKRAALCFRRNLGTYNRYKHYAPNKLCT 136
DB 59 PKRSTYSYSPQNGIVGCDQNLCKRAVCECDRAALCFGENVNTYDKYKDYPTSQCT 116

RESULT 8
ID PAZY_TRIFL STANDARD; PRT; 138 AA.
AC Q90Y77;
DT 28-FEB-2003 (Rel. 41; Created)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 10-OCT-2003 (Rel. 42; Last annotation update)
DE Phospholipase A2 isozyme PL-Y precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
SEQUENCE FROM N.A.
RA Chijiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
RA Nakashima K.-I., Oda-Ueda N., Shimohigashi Y., Fukumaki Y.,
RA Hattori S., Ohno M.;
RT "Regional evolution of Trimeresurus flavoviridis venom-gland
phospholipase A2 isozymes."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the
CC 2-acyl groups in 3-sn-phosphoglycerides (By similarity).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL; AB072173; BAB68546.1; -.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; 1.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolyase; Lipid degradation; Calcium; Multigene family; Signal.
FT SIGNAL 1 16 BY SIMILARITY.
FT CHAIN 17 138 PHOSPHOLIPASE A2 ISOZYME PL-Y.
FT ACT_SITE 63 63 BY SIMILARITY.
FT ACT_SITE 105 105 BY SIMILARITY.
FT DISULFID 42 131 BY SIMILARITY.
FT DISULFID 44 60 BY SIMILARITY.
FT DISULFID 59 111 BY SIMILARITY.
FT DISULFID 65 138 BY SIMILARITY.
FT DISULFID 66 104 BY SIMILARITY.
FT DISULFID 73 97 BY SIMILARITY.
FT DISULFID 91 102 BY SIMILARITY.
FT METAL 43 43 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 45 45 CALCIUM (BY SIMILARITY).
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 64 64 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 138 AA; 15729 MW; C96B1E878CCA1196 CRC64;

Query Match 43.9%; Score 358.5; DB 1; Length 138;
Best Local Similarity 47.4%; Pred. No. 4.8e-31;
Matches 65; Conservative 20; Mismatches 45; Indels 3; Gaps 2;

QY 7 LVFLCLLVALTGNLVQFGVMIKMTGKSGAL-QYNDYGVCGYGGSHWPDQTDWCCHAH 65
DB 4 LMIWAVLVGVGEGHLLQFRMKIKMTGKEPIVSFAFYGVCGYGGGKGRGPKDATDRCCFVH 63
QY 66 DCCYGRLEKLGCEPKLEKYLFSVSRGIFCAGETTCQRLTCECDKRAALCFRRNLGTYNR 125
DB 64 DCCYKLV--TGCDPKNDYTYTSLNGDIVCGDNPCTKVKVCECDKAAACFRDNLKITYK 121
QY 126 KYAHYPNKLCTGTPPC 142
DB 122 RYMTFPDIFCTDPTKTC 138

RESULT 9
ID PAZY_TRIFL STANDARD; PRT; 138 AA.
AC Q8UJGO;
DT 28-FEB-2003 (Rel. 41; Created)
DT 28-FEB-2003 (Rel. 41; Last sequence update)
DT 10-OCT-2003 (Rel. 42; Last annotation update)
DE Phospholipase A2 isozyme cPLA-B (A) precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN-Amami-Oshima, and Kagosima; TISSUE=Venom gland;
RX MEDLINE=22499762; PubMed=12612832;
RA Chijiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,
RA Nakashima K.-I., Oda-Ueda N., Fukumaki Y., Hattori S., Ohno M.;
RT "Interisland evolution of Trimeresurus flavoviridis venom
phospholipase A(2) isozymes."

```

J. Mol. Evol. 56:286-293(2003).

1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.

1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.

1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).

1- SUBCELLULAR LOCATION: Secreted (Probable).

1- TISSUE SPECIFICITY: Expressed by the venom gland.

1- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.

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EMBL; AB087496; BAC02719.1; -

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2c; 1.

DR PROSITE; PS00118; PA2\_HIS; 1.

DR Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.

KW SIGNAL 1 16

FT CHAIN 17 138

FT ACT\_SITE 63 63

FT ACT\_SITE 105 105

FT DISULFID 42 131

FT DISULFID 44 60

FT DISULFID 59 111

FT DISULFID 65 138

FT DISULFID 66 104

FT DISULFID 73 97

FT DISULFID 91 102

FT METAL 43 43

FT METAL 45 45

FT METAL 47 47

FT METAL 64 64

FT SEQUENCE 138 AA; 15703 MW; CDE540581DD2F10 CRC64;

Query Match 43.5%; Score 355.5; DB 1; Length 138;

Best Local Similarity 49.2%; Pred. No. 1e-30;

Matches 65; Conservative 17; Mismatches 47; Indels 3; Gaps 2;

Qy 12 LLVALVTGNLVFGVMLEKMTGKSL-QYNDYGCYCGIGGSHMPVDQTDWCHAHDCCYG 70

Db 9 VLLGVGELLQFRKMKTKGPKIVSVAFYFCYCGKGRGPKADTRCCFVHCCYG 68

Qy 71 RLEKLGCEPKLEKLYFVSERGIKFCAGRTTCORLTCECDKRAALCFRNLTGTYNRKYAHY 130

Db 69 KV--TGCDPKWDYTYSSENGDIVCEGDNPTCEVCECDKAAALCFRDLNLTGKYKRYMTF 126

Qy 131 PNKLTGTPPC 142

Db 127 PDIFCTDPTK 138

RESULT 10

PA2\_DABRR STANDARD; PRT; 121 AA.

AC P81458;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Phospholipase A2 RVV-VD (EC 3.1.1.4) (Phosphatidylcholine 2-

DE acylhydrolase).

OS Daboia russelli russelli (Russell's viper) (Vipera russelli russelli).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;

OC Viperidae; Viperinae; Daboia.

OX NCBI\_TaxID=31159;

RN [1]

RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).

RX TISSUE=Venom;

RX MEDLINE=98267643; PubMed=9604284;

RA Carredano E., Westerlund B., Persson B., Saarinen M., Ramaswamy S., Baker D., Eklund H.

RT "The three-dimensional structures of two toxins from snake venom throw light on the anticoagulant and neurotoxic sites of phospholipase A2.";

RL Toxicon 36:75-92(1998).

CC 1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. This protein has anticoagulant activity.

CC 1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.

CC 1- COFACTOR: Binds 1 calcium ion per subunit.

CC 1- SUBUNIT: Monomer.

CC 1- SUBCELLULAR LOCATION: Secreted.

CC 1- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.

CC PDB; 1VIP, 16-JUN-97.

DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; Phoslip; 1.

DR PRINTS; PR00389; PHPLIPASEA2.

DR ProDom; PD000303; PhospholipaseA2; 1.

DR SMART; SM00085; PA2c; 1.

DR PROSITE; PS00119; PA2c; 1.

DR PROSITE; PS00118; PA2\_HIS; 1.

DR Hydrolase; Lipid degradation; Calcium; 3D-structure.

KW ACT\_SITE 47 47

FT ACT\_SITE 89 89

FT DISULFID 26 115

FT DISULFID 28 44

FT DISULFID 43 95

FT DISULFID 49 121

FT DISULFID 50 88

FT DISULFID 57 81

FT DISULFID 75 86

FT METAL 27 27

FT METAL 29 29

FT METAL 31 31

FT METAL 48 48

FT METAL 2 13

FT HELIX 17 20

FT STRAND 23 24

FT TURN 25 27

FT STRAND 28 29

FT HELIX 39 53

FT TURN 54 54

FT HELIX 55 57

FT TURN 59 61

FT STRAND 66 68

FT STRAND 73 75

FT HELIX 80 98

FT TURN 99 102

FT HELIX 105 107

FT STRAND 108 108

FT TURN 109 109

FT HELIX 112 114

FT SEQUENCE 121 AA; 13626 MW; 98CBC4A8922A89D1 CRC64;

Query Match 43.5%; Score 355; DB 1; Length 121;

Best Local Similarity 53.2%; Pred. No. 9.9e-31;

Matches 66; Conservative 13; Mismatches 41; Indels 3;

```
QY 20 NLVQFGVMIEKMTGKSAL-QYNDYGCYCGIGSHWPDQTDWCHAHDCYGRLEKLGCE 78
Db 1 NLFQFAEMIVMTGKFLPSYSYDGYCGWGGKGPQDADRCFVHDCYKVK--SK 59
QY 79 PLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNRKAYHFNKLCCTGP 138
Db 59 PKLSLSYSPONGGIVCGDNHCKRAVCECDRAVATCFRNLNTYDKKYNHPPSQCTG- 117
QY 139 TTPC 142
Db 118 TEQC 121

RESULT 11
PA28 VIPPA STANDARD; PRT; 137 AA.
AC QYGGJ;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 homolog vp8 precursor.
OS Vipera palaestinae (Palaestine viper) (Pseudoceraastes palaestinae).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Vipera.
OX NCBI_TaxID=48068;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=99011427; PubMed=9792822;
RA Kordis D., Eotlan A., Gubensek F.;
RT "Positive darwinian selection in Vipera palaestinae phospholipase A2
RT genes is unexpectedly limited to the third exon."
RL Biochem. Biophys. Res. Commun. 251:613-619(1998).
CC -1- FUNCTION: Is not toxic by itself, but the synergistical mixture of
CC VP7 and VP8 is lethal to mice (By similarity).
CC -1- SUBUNIT: Does not form a complex (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).
CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF091854; AAC78084.1; -.
CC HSP; P81458; 1VIP.
CC InterPro; IPR001211; PhospholipaseA2.
CC Pfam; PF00068; phoslip; 1.
CC PRINTS; PR00389; PHPLIPASEA2.
CC ProDom; PD00303; PhospholipaseA2; 1.
CC SMART; SM00865; PA2C; 1.
CC PROSITE; PS00119; PA2_ASP; 1.
CC PROSITE; PS00118; PA2_HIS; 1.
KW Toxin; Signal; Multigene family.
FT SIGNAL 1 16
FT CHAIN 17 137
FT ACT_SITE 62 62
FT ACT_SITE 104 104
FT DISULFID 41 130
FT DISULFID 43 59
FT DISULFID 58 110
FT DISULFID 64 137
FT DISULFID 65 103
FT DISULFID 72 96
FT DISULFID 90 101
FT SEQUENCE 137 AA; 15349 MW; 281ACB6F82E103D9 CRC64;
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Query Match 43.3%; Score 354; DB 1; Length 137;
Best Local Similarity 54.5%; Fred.No. 1.4e-30;
Matches 66; Conservative 11; Mismatches 40; Indels 4; Gaps 2;

QY 7 LVFLCLLVALTGNLVQFGVMIEKMTGKSALQYNDYGCYCGIGSHWPDQTDWCHAHDC 66
Db 6 IVAVCLIG--VEGNLYQFGKMFVKTRKLSALSYDGYCGWGGKGPQDADRCFVHD 63
QY 67 CCYGRLEKLGCEPKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNRK 126
Db 64 CCYGTWN--GCDPKLSTYSYSPQNGDIVCGDDPCLRAVCECDRAVAALCFQENMNTYDK 121
QY 127 Y 127
Db 122 Y 122

RESULT 12
PA24 AGKHP STANDARD; PRT; 138 AA.
AC O42187;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 B precursor (SC 3.1.1.4) (Phosphatidylcholine 2-
DE acylhydrolase).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys
OS pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scieroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Gloydus.
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98353092; PubMed=9690782;
RA Pan H., Liu X.-L., Ou-Yang L.-L., Yang G.-Z., Zhou Y.-C., Li Z.-P.,
RA Wu X.-F.;
RT "Diversity of cDNAs encoding phospholipase A2 from Agkistrodon halys
RT pallas venom, and its expression in E. coli."
RL Toxicon 36:1155-1163(1998).
CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides (By similarity).
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -1- COFACTOR: Binds 1 calcium ion (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group II
CC subfamily.
CC
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CC
CC EMBL; AF015242; AAB71844.1; -.
CC FIR; JC1342; JC1342.
CC PDB; 1B4W; 12-JUN-98.
CC PDB; 1J1A; 10-JAN-98.
CC InterPro; IPR001211; PhospholipaseA2.
CC Pfam; PF00068; phoslip; 1.
CC PRINTS; PR00389; PHPLIPASEA2.
CC ProDom; PD00303; PhospholipaseA2; 1.
CC SMART; SM00865; PA2C; 1.
CC PROSITE; PS00119; PA2_ASP; 1.
CC PROSITE; PS00118; PA2_HIS; 1.
KW Lipid degradation; Hydrolase; Signal; Calcium; Multigene family;
FT SIGNAL 1 16
FT CHAIN 17 138
FT PHOSPHOLIPASE A2 B.
```



J. Protein Chem. 12:187-193(1993).  
[2]  
SEQUENCE OF 1-23, AND ACYLATION.  
TISSUE=Venom;  
MEDLINE=88298769; PubMed=3403524;  
RA Cho W., Tomasselli A.G., Heinrichson R.L., Kezdy F.J.;  
"The chemical basis for interfacial activation of monomeric  
phospholipases A2. Autocatalytic derivatization of the enzyme by acyl  
transfer from substrate.";  
J. Biol. Chem. 263:11237-11241(1988).  
[3]  
CHARACTERIZATION.  
TISSUE=Venom;  
MEDLINE=85054816; PubMed=6438084;  
RA Maraganore J.M., Merutka G., Cho W., Welches W., Kezdy F.J.,  
Heinrichson R.L.;  
"A new class of phospholipases A2 with lysine in place of aspartate  
49. Functional consequences for calcium and substrate binding.";  
J. Biol. Chem. 259:13839-13843(1984).  
[4]  
X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
TISSUE=Venom;  
MEDLINE=97166209; PubMed=9013608;  
RA Han S.X., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;  
"Structural aspects of interfacial adsorption. A crystallographic and  
site-directed mutagenesis study of the phospholipase A2 from the  
venom of Agkistrodon piscivorus piscivorus.";  
J. Biol. Chem. 272:3573-3582(1997).  
CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
acyl groups in 3-sn-phosphoglycerides.  
CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
acylglycerophosphocholine + a fatty acid anion.  
CC -1- COFACTOR: Binds 1 calcium ion per subunit.  
CC -1- SUBUNIT: Monomer or homodimer.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PM: Acylation causes dimerization.  
CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group II  
subfamily.  
DR PIR; B53872; B53872.  
DR PDB; 1VAP; 07-JUL-97.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR PRINTS; PR00389; PHPLIPASEA2.  
DR ProDom; PD00303; PhospholipaseA2; 1.  
DR SMART; SMO0085; PA2c; 1.  
DR PROSITE; PS00119; PA2 ASP; 1.  
DR PROSITE; PS00118; PA2 HIS; 1.  
KW Hydrolase; lipid degradation; Calcium; Lipoprotein; Palmitate;  
3D-structure.  
KW ACT\_SITE 47  
FT ACT\_SITE 47 BY SIMILARITY.  
FT ACT\_SITE 89 BY SIMILARITY.  
FT DISULFID 26  
FT DISULFID 28  
FT DISULFID 43  
FT DISULFID 49  
FT DISULFID 50  
FT DISULFID 57  
FT DISULFID 75  
FT METAL 27  
FT METAL 29  
FT METAL 31  
FT METAL 38  
FT METAL 48  
FT LIPID 7  
FT LIPID 10  
FT LIPID 12  
FT HELIX 13  
FT STRAND 17  
FT STRAND 23  
FT TURN 25  
FT TURN 28  
FT STRAND 29  
FT STRAND 39  
FT TURN 53  
FT TURN 59  
FT STRAND 66

FT TURN 70 71  
FT STRAND 72 75  
FT HELIX 80 98  
FT TURN 99 99  
FT HELIX 100 102  
FT HELIX 105 108  
FT STRAND 109 109  
FT TURN 110 110  
FT HELIX 113 116  
SQ SEQUENCE 123 AA; 13989 MW; C39986552D990D72 CRC64;  
Query Match 42.8%; Score 350; DB 1; Length 123;  
Best Local Similarity 52.0%; Pred. No. 3.4e-30;  
Matches 65; Conservative 14; Mismatches 42; Indels 4; Gaps 3;  
QY 20 NLVQFGVLEKMTGKSA-LQYNDYGCYCGIGSHHPVDOTDKCHAHDCCYCRLEKGC 78  
Db 1 NLFQFEKLIKMTGKSGMLWYSAYCYCGWGQGGPKDADRCCFVHDCCYGKV--TGCN 58  
QY 79 PKLEKLYFSVSRGIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRK-YAHYPNKLCTG 137  
Db 59 PMWDIYTVSDNGNIVCGTNPCKKQICECDRAAICFRDNLKTYDSKTYWYPKKNCKE 118  
QY 138 FPPPC 142  
Db 119 ESEPC 123  
RESULT 15  
PA2A\_MOUSE STANDARD; PRT; 146 AA.  
ID PA2A\_MOUSE  
AC P31482; Q60871;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)  
DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)  
DE (GIIC sPLA2) (Enhancing factor) (EF).  
DE GN PLA2G2A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALB/c;  
RA Mulherkar R.;  
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A., AND POLYMORPHISM.  
RC STRAIN=BALB/c, and CD-1; TISSUE=Intestine;  
RX MEDLINE=95403435; PubMed=7673223;  
RA Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,  
Yuan M., Tang C., Rancourt D.E., Cromlish W.;  
"A natural disruption of the secretory group II phospholipase A2 gene  
in inbred mouse strains";  
J. Biol. Chem. 270:22378-22385(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H;  
RX MEDLINE=95300227; PubMed=7781071;  
RA MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D.,  
Buchberg A.M.;  
"The secretory phospholipase A2 gene is a candidate for the Mom1  
locus, a major modifier of ApcMin-induced intestinal neoplasia.";  
Cell 81:957-966(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raba S.S., Loquellano N.A., Peters G.J., Abranino R.D., Mullaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,  
RA Schenck A., Schein J.E., Jones S.J.M., Marra M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 22-146 FROM N.A.  
RC STRAIN=BALB/c; TISSUE=Small intestine;  
RX MEDLINE=94029955; PubMed=8267767;  
RA Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;  
RT "Enhancing factor, a Paneth cell specific protein from mouse small  
intestines: predicted amino acid sequence from RT-PCR amplified cDNA  
and its expression.";  
RT Biochem. Biophys. Res. Commun. 195:1254-1263(1993).  
RN [6]  
RP ERRATUM.  
RX MEDLINE=94071967; PubMed=8250944;  
RA Mulherkar R., Rao R.S., Wagle A.S., Patki V., Deo M.G.;  
RL Biochem. Biophys. Res. Commun. 197:351-352(1993).  
RN [7]  
RP PRELIMINARY SEQUENCE OF 22-41.  
RC TISSUE=Small intestine;  
RX MEDLINE=93146172; PubMed=8425615;  
RA Mulherkar R., Rao R.S., Patki V., Chauhan V.S., Deo M.G.;  
RT "Enhancing factor protein from mouse small intestines belongs to the  
phospholipase A2 family.";  
RL FEBS Lett. 317:263-266(1993).  
CC -!- FUNCTION: May play a role in cell proliferation, by increasing the  
binding of EGF to the cells and thereby modulating its action. In  
doing so, this isozyme binds to a membrane-associated receptor  
distinct from the EGF receptor and which could be a heparan-  
sulfate proteoglycan located on the cell membrane.  
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
acyl groups in 3-sn-phosphoglycerides.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
acylglycerophosphocholine + a fatty acid anion.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
CC -!- SUBCELLULAR LOCATION: Membrane-associated.  
CC -!- TISSUE SPECIFICITY: Mainly in the Paneth cells adjacent to the  
stem population in the small intestines. Also expressed in  
regenerating liver and hyperplastic esophageal epithelium.  
CC -!- POLYMORPHISM: In strains 129/Sv, B10.RIII and C57BL/6, a  
polymorphism causes a frameshift and premature truncation of the  
protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1,  
DBA/2, MEL and NZB/B1N contain the normal protein while strain CD-  
1 is heterozygous for the mutation.  
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
-----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
between the Swiss Institute of Bioinformatics and the EMBL outstation -  
the European Bioinformatics Institute. There are no restrictions on its  
use by non-profit institutions as long as its content is in no way  
modified and this statement is not removed. Usage by and for commercial  
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
-----  
DR EMBL; X74266; CAA52325.1; -;  
DR EMBL; U32358; AAC52252.1; -;  
DR EMBL; U28244; AAB06315.1; ALT INIT.  
DR EMBL; BC045156; AAH45156.1; -;  
DR PIR; I48342; I48342.

DR PIR; S29495; S29495.  
DR HSP; P14555; IPOD.  
DR MGD; MGI:104642; P1a2g2a.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR PRINTS; PR00389; PHPLIPASEA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR SMART; SMO0085; PA2c; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
KW Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal;  
KW Membrane; Polymorphism.  
PT SIGNAL 1 21  
PT CHAIN 22 146  
FT ACT\_SITE 68 68  
FT ACT\_SITE 113 113  
FT DISULFID 47 139  
FT DISULFID 49 65  
FT DISULFID 64 119  
FT DISULFID 70 146  
FT DISULFID 71 112  
FT DISULFID 80 105  
FT DISULFID 98 110  
FT METAL 48 48  
FT METAL 50 50  
FT METAL 52 52  
FT METAL 69 69  
FT CONFLICT 19 19  
FT CONFLICT 86 86  
SQ SEQUENCE 146 AA; 16145 MW; AB904F6B3B1BA5C7 CRC64;  
Query Match 42.8%; Score 350; DB 1; Length 146;  
Best Local Similarity 53.1%; Pred. No. 4e-30;  
Matches 68; Conservative 9; Mismatches 49; Indels 2; Gaps 2;  
QY 17 VTGNLVQFGWIEKMTGKSA-LQYNDYCYGIGSHWPVDQDWCCCHADCCYGRLEKL 75  
DB 19 VQGNIAQFGEMIRLTKTKRAELSYAFYCHGLGKSGPKDATDRCCVTHDCCYKSLEKS 78  
QY 76 GCEPKLEKYLFSVSRGIFC-AGRTTCQRLTCBCDKRAALCFRRNLGTYNKRYAHYPNKL 134  
DB 79 GCGTKLLKYKSHQGGQITCSANQNSCQKRLCCQCDKAAAECAFARKKTKYSLKYQFPNMF 138  
QY 135 CTGPTTPC 142  
DB 139 CKGKPKC 146

Search completed: July 3, 2004, 05:16:39  
Job time : 10.1811 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:13:08 ; Search time 30.0075 Seconds  
(without alignments)  
1493.077 Million cell updates/sec

Title: US-10-088-092A-30  
Perfect score: 817  
Sequence: 1 MKSHVLVFLCLLVALVTGN.....YNRKYAHVPNKLCTGTPPC 142

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	361.5	44.2	146	11	Q91V34
2	342.5	41.9	138	13	Q7T1D5
3	339.5	41.6	138	13	Q805A3
4	337.5	41.3	138	13	Q8AXY1
5	337.5	41.3	138	13	Q805A2
6	330.5	40.5	138	13	Q7ZTA8
7	329.5	40.3	138	13	Q7ZTA6
8	328.5	40.2	138	13	Q7T1D1
9	327.5	40.1	138	13	Q7T1D4
10	327.5	40.1	138	13	Q7T1D3
11	327.5	40.1	138	13	Q7T1D2
12	322.5	39.5	138	13	Q800C1
13	321.5	39.4	138	13	Q800C2
14	321.5	39.4	138	13	Q7ZTA7
15	317.5	38.9	138	13	Q800C4
16	317.5	38.9	187	4	Q8N435

#### ALIGNMENTS

##### RESULT 1

Q91V34  
ID Q91V34 PRELIMINARY; PRT; 146 AA.  
AC Q91V34;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DE Platelet phospholipase A2 precursor (Fragment).  
OS Rattus norvegicus (Rat)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Wistar; TISSUE=Blood;  
RA Liu T.T., Liang N.S., Meng Z.Q., Xie Y.A., Kuang Z.P., Li Y.;  
RT "Cloning and sequence determination of rat platelet phospholipase A2 from whole blood."  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF365363; AAKS2061.1;  
DR GO; GO:0005509; P:calcium ion binding; IEA.  
DR GO; GO:0004623; P:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; Phoslip; 1.  
DR PRINTS; PR00389; PHPLIPASEA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR SMART; SM00085; PA2C; 1.  
DR PROSITE; PS00119; PA2 ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
KW Signal.  
FT SIGNAL 1 21  
FT CHAIN 22 >146  
FT NON\_TER 146 146  
SQ SEQUENCE 146 AA; 16306 MW; 60C1C9EC85DCBD67 CRC64;

Query Match 44.2%; Score 361.5; DB 11; Length 146;  
Best Local Similarity 47.9%; Pred. No. 2.4e-33;  
Matches 69; Conservative 18; Mismatches 50; Indels 7; Gaps 3;

Q7T2R1 vipera russ  
Q800C3 crotalus vi  
Q7Z3T5 vipera russ  
Q7Z3T5 vipera russ  
Q8N217 homo sapien  
Q804D7 bothrops ja  
Q8B193 mus musculu  
Q7T3S7 echis carin  
Q8CE14 mus musculu  
Q8X0Y1 mus musculu  
Q7T1C6 vipera aspi  
Q9X66 mesocricetu  
Q85Y6 mus musculu  
Q7Z60 rana catesb  
Q8AXW1 bungarus mu  
Q8AXW2 bungarus mu  
Q7T1R1 bungarus fl  
Q8AXW7 micrurus co  
Q8AXW8 bungarus ca  
Q8AXW0 bungarus mu  
Q8AXW0 pagrus majo  
Q7T2Q4 bungarus fl  
Q8WS88 adamsia car  
Q7T2Q5 bungarus fl  
Q802I1 bungarus ca  
Q9YH62 dicentrarch  
Q9U8P8 asterina pe  
O57313 pagrus majo



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DR PRINTS; PR00389; PPHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
SQ SEQUENCE 138 AA; 15456 MW; 513647907BFD0F4E CRC64;

Query Match 41.3%; Score 337.5; DB 13; Length 138;
Best Local Similarity 45.3%; Pred. No. 1.3e-30;
Matches 62; Conservative 19; Mismatches 53; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLVQFVMIKWTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAH 65
Db 4 LWIMAVLLVGVESLWFGKNTVMYMGESGLVQLSYGCVGGLGQOQPTDADRCCFVH 63

QY 66 DCCYGRLEKGCPEKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNR 125
Db 64 DCCYGVK--TDCNPKTASYTSENGEIVCGDDPKKQVCECDRAAIVCFGNLTATYKN 121

QY 126 KYAHVPNKLCTGTPPC 142
Db 122 KYMFGAKNCKESEP 138

RESULT 5
Q805A2 PRELIMINARY; PRT; 138 AA.
AC Q805A2
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PLA-N(O).
GN PLA2.
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=88087;
RN [1]
RP SEQUENCE FROM N.A.
RA Chijiwa T., Hamai S., Tsubouchi S., Ogawa T., Deshimaru M.,
RA Oda-Ueda N., Hattori S., Kihara H., Tsunazawa S., Ono M.;
RT "Interisland mutation of a novel phospholipase A2 from Trimeresurus
RT flavoviridis venom and evolution of crotalinae group II phospholipase
RT A2."
RL Submitted (EB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB102729; BAC56893.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PPHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
SQ SEQUENCE 138 AA; 15603 MW; A2F103123897ECC5 CRC64;

Query Match 41.3%; Score 337.5; DB 13; Length 138;
Best Local Similarity 47.4%; Pred. No. 1.3e-30;
Matches 65; Conservative 15; Mismatches 54; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLVQFVMIKWTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAH 65
Db 4 LWIMAVLLVGVESLWFGKNTVMYMGESGLVQLSYGCVGGLGQOQPTDADRCCFVH 63

QY 66 DCCYGRLEKGCPEKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNR 125
Db 64 DCCYGVK--TDCNPKTASYTSENGEIVCGDDPKKQVCECDRAAIVCFGNLTATYKN 121

QY 126 KYAHVPNKLCTGTPPC 142
Db 122 KYMFGAKNCKESEP 138
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Db 122 KYMFGDFLCTDPTKTC 138

RESULT 6
Q7ZTA8 PRELIMINARY; PRT; 138 AA.
AC Q7ZTA8
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acidic phospholipase A2.
OS Crotalus viridis viridis (Prairie rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8742;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;
RT "Geographic variations, cloning, and functional analyses of the venom
RT acidic phospholipases A2 of Crotalus viridis viridis."
RL Arch. Biochem. Biophys. 411:289-296(2003).
DR EMBL; AF120875; AA80563.1; -.
DR GO; GO:0005509; F:calcium ion binding; IEA.
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.
DR GO; GO:0016042; P:lipid catabolism; IEA.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PPHPLIPASEA2.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2c; 1.
DR PROSITE; PS00119; PA2 ASP; 1.
DR PROSITE; PS00118; PA2 HIS; 1.
SQ SEQUENCE 138 AA; 15414 MW; 44A35EA1FE6A39D0 CRC64;

Query Match 40.5%; Score 330.5; DB 13; Length 138;
Best Local Similarity 45.3%; Pred. No. 9e-30;
Matches 62; Conservative 18; Mismatches 54; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLVQFVMIKWTGKSA-LQYNDYGCYCGIGGSHWPVDQTDWCCHAH 65
Db 4 LWIMAVLLVGVESLWFGKNTVMYMGESGLVQLSYGCVGGLGQOQPTDADRCCFVH 63

QY 66 DCCYGRLEKGCPEKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRNLGTYNR 125
Db 64 DCCYGVK--TDCNPKTASYTSENGEIVCGDDPKKQVCECDRAAIVCFGNLTATYKN 121

QY 126 KYAHVPNKLCTGTPPC 142
Db 122 KYIQFPAKNCQEKPEPC 138

RESULT 7
Q7ZTA6 PRELIMINARY; PRT; 138 AA.
AC Q7ZTA6
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acidic phospholipase A2.
OS Crotalus viridis viridis (Prairie rattlesnake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Crotalus.
OX NCBI_TaxID=8742;
RN [1]
RP SEQUENCE FROM N.A.
RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;
RT "Geographic variations, cloning, and functional analyses of the venom
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DR PRINTS; PR00389; PHPLIPASEA2.  
DR PRODM; PD000303; PhospholipaseA2; 1.  
DR SMART; SM00085; PA2C; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
SQ SEQUENCE 138 AA; 15556 MW; 09134B8AB3EB3723 CRC64;

Query Match 39.4%; Score 321.5; DB 13; Length 138;  
Best Local Similarity 44.5%; Pred. No. 8.6e-29;  
Matches 61; Conservative 17; Mismatches 56; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLQVGVMIKTKSA-LQYNDYCYCGIGGSHWPVDQTDWCCHAH 65  
DB 4 LWIVAVLLGVGSLVQFETLIMKLAGSGLLWYSAYCYCGWGGHGLPQDATDCCFVH 63  
QY 66 DCCYGRLEKLCPEKLEKLYFSVSEIRGIFCAGRTTCORLTCECDKRAALCFRNLGTYNR 125  
DB 64 DCCYGVK--ATDCNPKTVSYTYSENGEIVCGDNPCCGTQICECDKAAICFRDNPISYN 121  
QY 126 KYAHYPNKLCTGTPPC 142  
DB 122 NYKFFPAENCRGDPEPC 138

## RESULT 14

Q7ZTA7 PRELIMINARY; PRT; 138 AA.

AC Q7ZTA7;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE -Acidic phospholipase A2.  
OS Crotalus viridis viridis (Prairie rattlesnake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Crotalus.  
ON NCBI\_TaxID=8742;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E6a;  
RX MEDLINE=22510024; PubMed=12623078;

RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;  
RT "Geographic variations, cloning, and functional analyses of the venom  
RT acidic phospholipases A2 of Crotalus viridis viridis.";  
RL Arch. Biochem. Biophys. 411:289-296(2003).

DR EMBL; AY120876; RAB0564.1;  
DR GO; GO:0005509; F:calcium ion binding; IEA.  
DR GO; GO:0004623; F:phospholipase A2 activity; IEA.  
DR GO; GO:0016042; P:lipid catabolism; IEA.  
DR InterPro; IPR001211; PhospholipaseA2.

DR Pfam; PF00068; phoslip; 1.  
DR PRINTS; PS00389; PHPLIPASEA2.  
DR PRODM; PD000303; PhospholipaseA2; 1.  
DR SMART; SM00085; PA2C; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
SQ SEQUENCE 138 AA; 15549 MW; 04FF6D7266D80BFE CRC64;

Query Match 39.4%; Score 321.5; DB 13; Length 138;  
Best Local Similarity 43.8%; Pred. No. 8.6e-29;  
Matches 60; Conservative 20; Mismatches 54; Indels 3; Gaps 2;

QY 7 LVFLCLLVALVTGNLQVGVMIKTKSA-LQYNDYCYCGIGGSHWPVDQTDWCCHAH 65  
DB 4 LWIVAVLLGVGSLVQFETLIMKLAGSGLLWYSAYCYCGWGGHGLPQDATDCCFVH 63  
QY 66 DCCYGRLEKLCPEKLEKLYFSVSEIRGIFCAGRTTCORLTCECDKRAALCFRNLGTYNR 125  
DB 64 DCCYGVK--TDCNPKTVSYTYSENGEIVCGDNPCCGTQICECDKAAICFRDNPISYN 121  
QY 126 KYAHYPNKLCTGTPPC 142  
DB 122 KYWFFPENCQEEPEPC 138

## RESULT 15

Q800C4 PRELIMINARY; PRT; 138 AA.

AC Q800C4;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Phospholipase A2.  
OS Crotalus viridis viridis (Prairie rattlesnake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Crotalus.  
ON NCBI\_TaxID=8742;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E6a;  
RX MEDLINE=22510024; PubMed=12623078;  
RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;  
RT "Geographic variations, cloning, and functional analyses of the venom  
RT acidic phospholipases A(2) of Crotalus viridis viridis.";  
RL Arch. Biochem. Biophys. 411:289-296(2003).

## RESULT 16

Q800C4 PRELIMINARY; PRT; 138 AA.

AC Q800C4;  
DT 01-JUN-2003 (TRENBLrel. 24, Created)  
DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
DE Phospholipase A2.  
OS Crotalus viridis viridis (Prairie rattlesnake).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Crotalus.  
ON NCBI\_TaxID=8742;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E6a;  
RX MEDLINE=22510024; PubMed=12623078;  
RA Tsai I.-H., Wang Y.-M., Chen Y.-H., Tu A.T.;  
RT "Geographic variations, cloning, and functional analyses of the venom  
RT acidic phospholipases A(2) of Crotalus viridis viridis.";  
RL Arch. Biochem. Biophys. 411:289-296(2003).

QY 7 LVFLCLLVALVTGNLQVGVMIKTKSA-LQYNDYCYCGIGGSHWPVDQTDWCCHAH 65  
DB 4 LWIVAVLLGVGSLVQFETLIMKLAGSGLLWYSAYCYCGWGGHGLPQDATDCCFVH 63  
QY 66 DCCYGRLEKLCPEKLEKLYFSVSEIRGIFCAGRTTCORLTCECDKRAALCFRNLGTYNR 125  
DB 64 DCCYGVK--ATDCNPKTVSYTYSENGEIVCGDNPCCGTQICECDKAAICFRDNPISYN 121  
QY 126 KYAHYPNKLCTGTPPC 142  
DB 122 KYWFFPENCQEEPEPC 138

Search completed: July 3, 2004, 05:17:44  
Job time : 33.0075 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:12:17 ; Search time 40.1887 Seconds  
(without alignments)  
998.335 Million cell updates/sec

Title: US-10-088-092a-30  
Perfect score: 817  
Sequence: 1 MKSPHVLVFLCLVALVTGN.....YNRKYAHYPNKLCTGTPPPC 142

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003as:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	817	100.0	142	4	AAB81022
2	817	100.0	154	6	ABR44235 Human pro
3	817	100.0	154	6	ABU63125 Human gro
4	709	86.8	142	3	AAB12810 Mouse sec
5	709	86.8	142	4	AAB81021 Murine ph
6	370	45.3	164	3	AAB56432 Human pro
7	368.5	45.1	144	1	AAP93112 Human inf
8	368.5	45.1	144	1	AAP93112 Human syn
9	368.5	45.1	144	2	AAR25416 PLA2. 1/1
10	368.5	45.1	144	2	AAR63055 Human PLA
11	368.5	45.1	144	6	ABR44233 Human sec
12	368.5	45.1	144	6	ABP96807 Human pro
13	368.5	45.1	144	6	ABU63123 Human gro
14	368.5	45.1	144	7	ADB75501 Prostato
15	368.5	45.1	144	7	ADE63560 Human pro
16	363.5	44.5	124	6	ADA61984 Human I8M
17	360.5	44.1	124	2	AAAR10126 Membrane-
18	360.5	44.1	124	2	AAW73562 Human gro
19	360.5	44.1	124	6	ADA61982 Human G72
20	360.5	44.1	124	6	ADA61978 Human G72
21	360.5	44.1	124	6	ABR93558 Human PLA
22	359.5	44.0	146	7	ADE63558 Rat Prote
23	357.5	43.8	124	6	ADA61983 Human T10
24	351	43.0	145	2	AAR63053 HPLA2-8.
25	350	42.8	146	2	AAW08368 Mouse PLA

26	350	42.8	146	5	ABR08154	Ab08154 Murine PL
27	350	42.8	146	6	ABP96808	Abp96808 Mouse pro
28	348	42.6	125	2	AAS63060	Aas63060 Rat PLA2
29	331.5	40.6	122	3	AAV88292	Aay88292 Agkistrod
30	329	40.3	144	3	AAI12536	Aab12536 Mouse sec
31	329	40.3	144	3	AAI11994	Aab11994 Mouse sec
32	317.5	38.9	138	2	AAR63046	Aar63046 HPLA2-10.
33	317.5	38.9	138	6	ABR44237	AbR44237 Human sec
34	317.5	38.9	138	6	AAE37571	Aae37571 Human pro
35	317.5	38.9	138	6	ABU63126	Abu63126 Human gro
36	317.5	38.9	138	7	ADP47911	Add47911 Human pro
37	317.5	38.9	138	7	ADB47915	Add47915 Human pro
38	317.5	38.9	138	7	ADD47919	Add47919 Human pro
39	314.5	38.5	132	2	AAW58476	Aaw58476 Human syn
40	314.5	38.5	137	2	AAR63045	Aar63045 RPLA2-10.
41	314.5	38.5	137	7	ADD47917	Add47917 Rat Prote
42	314.5	38.5	137	7	ADD47909	Add47909 Rat Prote
43	314.5	38.5	137	7	ADD47913	Add47913 Rat Prote
44	310.5	38.0	145	4	AAU09096	Aau09096 Novel hum
45	310.5	38.0	145	6	ABR44234	AbR44234 Human sec

## ALIGNMENTS

RESULT 1  
AAB81022  
ID AAB81022 standard; protein; 142 AA.  
XX  
AC AAB81022;  
XX  
DT 12-JUN-2001 (first entry)  
XX  
DE Human phospholipase A2 (PLA2) amino acid sequence.  
XX  
KW Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnary;  
KW antiinflammatory; tranquiliser; antischmatic; antiallergic; trauma;  
KW antirheumatic; antiarthritic; septic shock; pancreatitis; human;  
KW adult respiratory distress syndrome; ARDS; bronchial asthma;  
KW allergic rhinitis; rheumatoid arthritis.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..19  
FT Protein /label= Signal\_peptide  
FT /label= Mature PLA2  
FT /note= "Mature phospholipase A2"  
FT  
FT WO200121775-A1.  
XX  
XX 29-MAR-2001.  
XX  
XX 18-SEP-2000; 2000WO-JP006344.  
XX  
XX 21-SEP-1999; 99JP-00266616.  
XX (SHIO ) SHIONOGI & CO LTD.  
XX  
XX Ishizaki J, Suzuki N, Harasaki K;  
DR WPI; 2001-290432/30.  
DR N-PSDB; AAF77401.  
XX  
XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis of  
XX and screening drug candidates for treating associated diseases e.g.  
XX septic shock, adult respiratory distress syndrome and rheumatoid  
XX arthritis.  
XX  
XX Claim 1; Page 46-47; 50pp; Japanese.  
XX  
XX This invention relates to human secretory phospholipase A2 (PLA2) protein

CC and the gene encoding it. Inhibitors of phospholipase A2 have  
 CC antibacterial; immunosuppressive; antiinflammatory; tranquilizer;  
 CC vulnary; antiasthmatic; antiallergic; antirheumatic; and antiarthritic  
 CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in  
 CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult  
 CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,  
 CC allergic rhinitis and rheumatoid arthritis. The present sequence  
 CC represents human PLA2  
 XX  
 SQ Sequence 142 AA;

Query Match 100.0%; Score 817; DB 4; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-67;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIKMTGKSAIQNDYGCYGGSHWPDQTDW 60  
 DB 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIKMTGKSAIQNDYGCYGGSHWPDQTDW 60  
 QY 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSEGIKMTGKSAIQNDYGCYGGSHWPDQTDW 120  
 DB 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSEGIKMTGKSAIQNDYGCYGGSHWPDQTDW 120  
 QY 121 GTYNRYAHYPNKLTGTPPC 142  
 DB 121 GTYNRYAHYPNKLTGTPPC 142

RESULT 2  
 ABR44235  
 ID ABR44235 standard; protein; 154 AA.  
 XX  
 AC ABR44235;  
 XX  
 DT 18-AUG-2003 (first entry)  
 XX  
 DE Human secreted group IIE phospholipase A2 (sPLA2) enzyme.

XX Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;  
 KW phosphatidylcholine; antibacterial; virucide; cytostatic; vasotropic;  
 KW antiinflammatory; vulnary; cardiant; chromosome lp35; transgenic;  
 KW enzyme.

XX Homo sapiens.  
 XX WO2003033689-A1.

XX 24-APR-2003.

XX 12-OCT-2001; 2001WO-IB002407.

XX 12-OCT-2001; 2001WO-IB002407.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Lazdunski M, Lambeau G, Valentin E;

XX WPI; 2003-403216/38.

XX Novel mammalian secreted group IIF secreted phospholipase A2, useful for  
 PT preventing and treating bacterial and viral infections, and cancers.

XX Disclosure; Fig 1; 33pp; English.

XX The invention relates to a mammalian secreted group IIF secreted  
 CC phospholipase A2 (sPLA2) (I), where the enzyme is Ca<sup>2+</sup> dependent,  
 CC maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus  
 CC phosphatidylcholine with a 15-fold preference. A pharmaceutical  
 CC composition comprising (I) is useful for treating or preventing viral and  
 CC bacterial infections, and cancers. A pharmaceutical composition  
 CC containing compounds capable of inhibiting catalytic activity of (I),  
 CC biologically active compounds that bind sPLA2 receptors, or a compound  
 CC that modulates cell proliferation, cell migration, cell contraction or

CC apoptosis is useful for treating disease states or disorders involving  
 CC group IIF sPLA2, such as inflammatory disease, cancers, cardiac and brain  
 CC ischaemia, acute lung injury, acute respiratory distress syndrome or  
 CC Crohn's disease. Specific antibodies are useful for searching new  
 CC secreted mammalian group IIF sPLA2 or the homologues of the enzyme in  
 CC other mammals. The encoding polynucleotides and vectors are useful for  
 CC transforming animals and establishing a line of transgenic animals.  
 CC Sequences ABR4232-238 represent various human secreted sPLA2 enzymes  
 CC used in alignment studies with the GIIIF sPLA2 enzyme  
 XX  
 SQ Sequence 154 AA;

Query Match 100.0%; Score 817; DB 6; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-67;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIKMTGKSAIQNDYGCYGGSHWPDQTDW 60  
 DB 13 MKSPHVLVFLCLLVALVTGNLVQFGVMIKMTGKSAIQNDYGCYGGSHWPDQTDW 72  
 QY 61 CCHADCCYGRLEKLGCEPKLEKYLFSVSEGIKMTGKSAIQNDYGCYGGSHWPDQTDW 120  
 DB 73 CCHADCCYGRLEKLGCEPKLEKYLFSVSEGIKMTGKSAIQNDYGCYGGSHWPDQTDW 132  
 QY 121 GTYNRYAHYPNKLTGTPPC 142  
 DB 133 GTYNRYAHYPNKLTGTPPC 154

RESULT 3  
 ABR63125  
 ID ABR63125 standard; protein; 154 AA.

XX ABR63125;  
 XX  
 DT 25-SEP-2003 (first entry)

XX Human group IIE secreted phospholipase A2.

XX Human; group IIE secreted phospholipase A2; virucide; antibacterial;  
 KW cytostatic; antiinflammatory; vasotropic; cerebroprotective; sPLA2;  
 KW phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;  
 KW viral infection; bacterial infection; cancer; inflammatory disease;  
 KW cardiac ischaemia; brain ischaemia; acute lung injury;  
 KW acute respiratory distress syndrome; Crohn's disease; enzyme.

XX Homo sapiens.

XX US2003073087-A1.

XX 17-APR-2003.

XX 11-OCT-2001; 2001US-00975456.

XX 11-OCT-2000; 2000US-0239491P.

XX (LAZD/) LAZDUNSKI M.

XX (LAMB/) LAMBEAU G.

XX (VALE/) VALENTIN E.

XX Lazdunski M, Lambeau G, Valentin E;

XX WPI; 2003-567302/53.

XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful  
 PT for treating or preventing viral or bacterial infections, or cancers, or  
 PT screening inhibitors of the enzyme for treating e.g. inflammatory  
 PT diseases or ischemia.

XX Disclosure; Fig 1; 16pp; English.

XX The invention describes a mammalian secreted group IIF phospholipase A2  
 CC (sPLA2), which is Ca<sup>2+</sup>-dependent, maximally active at pH of about 7-8,



CC and hydrolyses phosphatidylglycerol versus phosphatidylcholine with about  
 CC a 15-fold preference. The mammalian secreted group IIP sPLA2 protein or  
 CC nucleic acid, or a pharmaceutical composition is useful for treating  
 CC and/or preventing viral infections, bacterial infections, or cancers. The  
 CC inhibitors of sPLA2 or a composition comprising sPLA2 inhibitors is  
 CC useful for treating disease states or disorders involving group IIP  
 CC sPLA2, e.g. inflammatory diseases, cancer, cardiac and brain ischaemia,  
 CC acute lung injury, acute respiratory distress syndrome, or Crohn's  
 CC disease. The enzyme is also useful for screening various chemical  
 CC compounds for treating these diseases. This is the amino acid sequence of  
 CC human group IIE phospholipase A2 used to determine a consensus sequence  
 CC for human sPLA2s

XX Sequence 154 AA;

Query Match 100.0%; Score 817; DB 6; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 1.6e-67;  
 Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSAIQYNDYGCYGGSHWPDQTDW 60  
 DB 13 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSAIQYNDYGCYGGSHWPDQTDW 72  
 QY 61 CCHAHDCCYGRLEKLGCEPKLEKLFVSVERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120  
 DB 73 CCHAHDCCYGRLEKLGCEPKLEKLFVSVERGIFCAGRTTCQRLTCECDKRAALCFRRNL 132  
 QY 121 GTYNRYAHYPNKLCTGTPPPC 142  
 DB 133 GTYNRYAHYPNKLCTGTPPPC 154

#### RESULT 4

AAB12810  
 ID AAB12810 standard; protein; 142 AA.

AC AAB12810;

DT 27-NOV-2000 (first entry)

DE Mouse secretory type phospholipase A2 protein SEQ ID NO:15.

XX Mouse; secretory phospholipase A2; PLA2; screening; development;  
 XX inhibitor.

OS Mus musculus.

PN JP2000166568-A.

XX 20-JUN-2000.

XX 09-DEC-1998; 98JP-00349604.

XX 09-DEC-1998; 98JP-00349604.

XX (SHIO ) SHIONOGI & CO LTD.

XX WPI; 2000-485554/43.

XX N-PSDB; AAA73130.

XX New gene encoding mouse secretory type phospholipase A2 (PLA2) for  
 PT screening for inhibitors of PLA2.

PS Claim 1; Page 13-14; 15pp; Japanese.

XX The present invention describes a mouse secretory type phospholipase A2  
 CC (PLA2) protein. The mouse secretory type PLA2-like protein can be used  
 CC for screening in the development of inhibitors against the function of  
 CC the protein. The present sequence represents mouse secretory type PLA2

XX Sequence 142 AA;

Query Match

86.8%; Score 709; DB 3; Length 142;

Best Local Similarity 84.5%; Pred. No. 1.3e-57;  
 Matches 120; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 MKSPHVLVFLCLLVALVTGNLVQFGVMIEKMTGKSAIQYNDYGCYGGSHWPDQTDW 60  
 DB 1 MKPPIALACLLVPLAGGNLVQFGVMIEKMTGKSAIQYNDYGCYGGSHWPDQTDW 60

QY 61 CCHAHDCCYGRLEKLGCEPKLEKLFVSVERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120

DB 61 CCHAHDCCYGRLEKLGCEPKLEKLFVSVERGIFCAGRTTCQRLTCECDKRAALCFRRNL 120

QY 121 GTYNRYAHYPNKLCTGTPPPC 142

DB 121 NTYNRYAHYPNKLCTGTPPPC 142

#### RESULT 5

AAB81021

ID AAB81021 standard; protein; 142 AA.

AC AAB81021;

DT 12-JUN-2001 (first entry)

DE Murine phospholipase A2 (PLA2) amino acid sequence.

XX Phospholipase A2; PLA2; antibacterial; immunosuppressive; vulnery;  
 XX antiinflammatory; tranquilliser; antiaesthetic; antiallergic; trauma;  
 KW antirheumatic; antiarthritic; septic shock; pancreatitis; mouse;  
 KW adult respiratory distress syndrome; ARDS; bronchial asthma;  
 KW allergic rhinitis; rheumatoid arthritis.

OS Mus musculus.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= Signal\_peptide

FT 20..142

FT /label= Mature\_PLA2

FT /note= "Mature phospholipase A2"

XX WO200121775-A1.

XX 29-MAR-2001.

XX 18-SEP-2000; 2000WO-JP006344.

XX 21-SEP-1999; 99JP-00266616.

XX (SHIO ) SHIONOGI & CO LTD.

XX Ishizaki J, Suzuki N, Hanasaki K;

XX WPI; 2001-290432/30.

XX N-PSDB; AAF77387.

XX Human secretory phospholipase A2 and encoded gene, useful in diagnosis of  
 PT and screening drug candidates for treating associated diseases e.g.  
 PT septic shock, adult respiratory distress syndrome and rheumatoid  
 PT arthritis.

XX Example 3; Page 42; 50pp; Japanese.

XX This invention relates to human secretory phospholipase A2 (PLA2) protein  
 CC and the gene encoding it. Inhibitors of phospholipase A2 have  
 CC antibacterial; immunosuppressive; antiinflammatory; tranquilliser;  
 CC vulnery; antiaesthetic; antiallergic; antirheumatic; and antiarthritic  
 CC activity. The PLA2 protein, gene and an anti-PLA2 antibody are useful in  
 CC the diagnosis of PLA2 associated diseases e.g. septic shock, adult  
 CC respiratory distress syndrome, pancreatitis, trauma, bronchial asthma,  
 CC allergic rhinitis and rheumatoid arthritis. The present sequence  
 CC represents murine PLA2. The murine PLA2 gene sequence is used in the  
 CC invention for the identification and characterisation of the human PLA2



PA (BIOJ ) BIOGEN INC.  
 XX Kramer RM, Pepinsky R, Hession C;  
 XX WPI; 1989-324225/44.  
 DR N-PSDB; AAN91825, AAN97209.  
 XX Acid stable phospholipase A2 - used for prodn. of antibodies and in the  
 PT treatment or diagnosis of inflammation and other diseases.  
 XX Claim 44; Fig 12; 84pp; English.  
 XX The protein sequence was deduced from a DNA sequence obtd. from a genomic  
 CC DNA library which was prepd. from a mutant fibroblast cell line which  
 CC contains 5 copies of the X chromosome (GM5009). The signal sequence is  
 CC thought to be incomplete at the N-terminal since no promoter-like  
 CC sequences are found in the DNA within 100 nucleotides 5' of this  
 CC region. The deduced N-terminal sequence of the mature protein confirmed  
 CC results obtd. by direct sequencing of the purified protein. This sequence  
 CC represents an amphiphilic alpha-helix typical of PLA 2 mols. It has  
 CC highly conserved lipophilic residues [e.g. Leu (22), Phe (25), and Ile  
 CC (29)] and there is a cluster of basic amino acids [e.g. Arg (27), Lys  
 CC (30) and Lys (35)] which is believed to be an important determinant in  
 CC the interaction of PLA 2. There is a characteristic stretch of residues  
 CC which comprises part of the calcium binding loop: Tyr(44)-Gly-Cys-X-Cys-  
 CC Gly-X-Gly-X-X-Pro(58) and Asp(68). The conserved residues which  
 CC constitute the active site (see features) are also present, and the  
 CC protein exhibits the placement of half-cysteine residues typical of a Gp  
 CC II PLA 2, having a Cys residue at position 70 and a half cysteine at the  
 CC C-terminal. (The consensus sequence was determined from a comparison of  
 CC PLA 2s from bovine pancreas and C. atrox venom. (Updated on 25-MAR-2003  
 CC to correct PR field.)  
 XX - Sequence 144 AA;  
 SQ Query Match 45.1%; Score 368.5; DB 1; Length 144;  
 Best Local Similarity 52.1%; Pred. No. 3.2e-26;  
 Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;  
 QY 12 LLVALVT-----GNLVQFGVMIERMTGK-SALQYNDYGCYCGIGGSHWPDQTDWCC 62  
 Db 5 LLLAVIMIFGLLQAHGNLVNFRHMIKLTGTKEAALSYGYGCHGCVGGSGPKDATDRCC 64  
 QY 63 HAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFERNLGT 122  
 Db 65 VTHDCCYRLEKRCGCTKFLSYKFSNSGSRITCAKQDSQRSQLECDKAAATCFARNKTT 124  
 QY 123 YNRKYAHYPNKLCTGTPPC 142  
 Db 125 YNKYQYYSNKHCRGSTPRC 144  
 RESULT 8  
 AAR25416  
 ID AAR25416 standard; protein; 144 AA.  
 XX AAR25416;  
 AC AAR25416;  
 XX 25-MAR-2003 (revised)  
 DT 27-JUN-1980 (first entry)  
 XX Human synovial phospholipase type A2 (sPLA2) as encoded by cDNA clone  
 DE lambda SPLA2cDNA-4 and by the exons of clone lambda SPLA2-6.  
 XX Human synovial phospholipase A2; clone lambda SPLA2cDNA-4;  
 KW lambda SPLA2-6.  
 XX Homo sapiens.  
 OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Protein 21..144  
 XX WO8901773-A.

XX 09-MAR-1989.  
 XX 23-AUG-1988; 88WO-US002896.  
 XX 27-AUG-1987; 87US-00089883.  
 PR 06-JUL-1988; 88US-00215726.  
 PR 16-AUG-1988; 88US-00231865.  
 XX (BIOT-) BIOTECHN RES PARTN.  
 PA (UTOR ) UNIV OF TORONTO INNOVAT.  
 XX Johnson LX, Seilhamer JJ, Pruzanski W, Vadas P;  
 PI WPI; 1989-085394/11.  
 DR N-PSDB; AAN91258, AAN91260.  
 XX Mammalian synovial phospholipase A2 - used in food processing, design and  
 PT screening of inflammation inhibitors, as an anticancer drug or vaccine  
 PT adjuvant etc.  
 XX Disclosure; Fig 6; 70pp; English.  
 XX Clone lambda SPLA2cDNA-4 is one of four clones identified when probe  
 CC oligo 2905 (AAN91257) was used to screen a cDNA library constructed from  
 CC polyA+ message from a peritoneal cell RNA. It encodes the entire SPLA2  
 CC type A sequence which is given here. The mature peptide sequence (see PT)  
 CC has a calculated molecular weight of 13,919 daltons. The same amino acid  
 CC sequence is also encoded by the exons of clone lambda SPLA2-6 (AAN91260)  
 CC in figure 7. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25  
 CC -MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI  
 CC field.)  
 XX - Sequence 144 AA;  
 SQ Query Match 45.1%; Score 368.5; DB 1; Length 144;  
 Best Local Similarity 52.1%; Pred. No. 3.2e-26;  
 Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;  
 QY 12 LLVALVT-----GNLVQFGVMIERMTGK-SALQYNDYGCYCGIGGSHWPDQTDWCC 62  
 Db 5 LLLAVIMIFGLLQAHGNLVNFRHMIKLTGTKEAALSYGYGCHGCVGGSGPKDATDRCC 64  
 QY 63 HAHDCCYGRLEKLGCEPKLEKYLFSVSERGIFCAGRTTCORLTCECDKRAALCFERNLGT 122  
 Db 65 VTHDCCYRLEKRCGCTKFLSYKFSNSGSRITCAKQDSQRSQLECDKAAATCFARNKTT 124  
 QY 123 YNRKYAHYPNKLCTGTPPC 142  
 Db 125 YNKYQYYSNKHCRGSTPRC 144  
 RESULT 9  
 AAR25416  
 ID AAR25416 standard; protein; 144 AA.  
 XX AAR25416;  
 AC AAR25416;  
 XX 06-JAN-1993 (first entry)  
 DT PLA2.  
 DE Human growth hormone; granulocyte-colony stimulating factor; G-CSF;  
 KW phospholipase A2; HGH; PCR; polymerase chain reaction; gene therapy;  
 KW erythroid cells; cDNA library.  
 XX Synthetic.  
 OS Synthetic.  
 XX GB2251622-A.  
 XX 15-JUL-1992.  
 PD 19-DEC-1991; 91GB-00026984.  
 XX PF

XX 21-DEC-1990; 90GB-00027917.  
 XX (ICIL ) IMPERIAL CHEM IND PLC.  
 XX Hollis M, Needham MRC, Gooding C, Grosveld FG, Antoniou M;  
 XX WPI; 1992-236158/29.  
 XX N-PSDB; AAQ26372.  
 XX Expression vectors for use in mammalian cells - contain dominant control  
 XX region derived from beta-globin gene.  
 XX Disclosure; Fig 11; 77pp; English.  
 XX This sequence is encoded by the phospholipase A2 (PLA2) cDNA. The cDNA  
 XX was amplified using the primer sequences given in AAQ26370-1 by PCR from  
 XX a human lung cDNA library. The cDNA sequence was used in the construction  
 XX of an expression vector which further comprised a promoter and a dominant  
 XX control region. This vector was used in an expression system comprising a  
 XX mammalian cell transformed with the vector. This expression system could  
 XX be used to prepare pharmacologically useful polypeptides eg. human growth  
 XX hormone (HGH), granulocyte-colony stimulating factor (G-CSF) and PLA2,  
 XX and for gene therapy. The mammalian host comprises erythroid cells and a  
 XX heterologous promoter  
 XX Sequence 144 AA;  
 XX  
 Query Match 45.1%; Score 368.5; DB 2; Length 144;  
 Best Local Similarity 52.1%; Pred. No. 3.2e-26;  
 Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;  
 QY 12 LLVALVT-----GNLVQGVMIKMTGK-SALQYNDYGCYIGGSHWPDQTDWCC 62  
 DB 5 LLLAVIMIFGLLQAHGNLWVNFHRIKLTGKEAALSFGYCHGCGVGRGSPKDATDRCC 64  
 QY 63 HAHDCYGRLEKLGCEPKLEKLFVSBERGIFCAGRTTCQRLTCECDKRAALCFRRNLGT 122  
 DB 65 VTHDCCYKLEKRGCGGKTFLSYKFSNSGSRITCAKQDSCRQSCQLCECDKAAATCFARNKTT 124  
 QY 123 YNRKYAHYFNKLTGPTTPPC 142  
 DB 125 YNKYQYYSNKHCRGSTPRC 144  
 RESULT 10  
 AAR63055  
 ID AAR63055 standard; protein; 144 AA.  
 AC AAR63055;  
 DT 25-MAR-2003 (revised)  
 DT 15-AUG-1995 (first entry)  
 XX Human PLA2 type II.  
 DE HPLA2-10; phospholipase A2; PLA2.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 PN WO9502328-A1.  
 PD 26-JAN-1995.  
 PF 15-JUL-1994; 94WO-US007926.  
 PR 15-JUL-1993; 93US-00091941.  
 PR 26-JUL-1993; 93US-00097354.  
 PA (INDV ) UNIV INDIANA FOUND.  
 PA (INCY-) INCYTE PHARM INC.  
 XX Tischfield JA, Seilhamer JJ;

XX WPI; 1995-067096/09.  
 XX Novel type III and IV low mol. wt. phospholipase A2 enzymes - from humans  
 XX and rats, also nucleic acid sequences useful, e.g. for recombinant prodn.  
 XX of enzymes, research into Batten's disease, etc.  
 XX Disclosure; Fig 15; 160pp; English.  
 XX A human cDNA (AAQ81138) expressing a novel PLA2, HPLA2-10, was derived  
 XX from human brain RNA by RACE-PCR. HPLA2-10 (AAR63046) was characterized  
 XX as a novel type of PLA2, type IV, on the basis of its Cys content in  
 XX comparison with human PLA2 types I (AAR63054) and II (AAR63055) (Updated  
 XX on 25-MAR-2003 to correct PN field.)  
 XX Sequence 144 AA;  
 XX  
 Query Match 45.1%; Score 368.5; DB 2; Length 144;  
 Best Local Similarity 52.1%; Pred. No. 3.2e-26;  
 Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;  
 QY 12 LLVALVT-----GNLVQGVMIKMTGK-SALQYNDYGCYIGGSHWPDQTDWCC 62  
 DB 5 LLLAVIMIFGLLQAHGNLWVNFHRIKLTGKEAALSFGYCHGCGVGRGSPKDATDRCC 64  
 QY 63 HAHDCYGRLEKLGCEPKLEKLFVSBERGIFCAGRTTCQRLTCECDKRAALCFRRNLGT 122  
 DB 65 VTHDCCYKLEKRGCGGKTFLSYKFSNSGSRITCAKQDSCRQSCQLCECDKAAATCFARNKTT 124  
 QY 123 YNRKYAHYFNKLTGPTTPPC 142  
 DB 125 YNKYQYYSNKHCRGSTPRC 144  
 RESULT 11  
 ABR44233  
 ID ABR44233 standard; protein; 144 AA.  
 AC ABR44233;  
 DT 18-AUG-2003 (first entry)  
 XX Human secreted group IIA phospholipase A2 (sPLA2) enzyme.  
 DE Group IIF secreted phospholipase A2; sPLA2; phosphatidylglycerol; human;  
 KW phosphatidylcholine; antibacterial; virucide; cytostatic; vasotropic;  
 KW antiinflammatory; vulnery; cardiant; chromosome 1p35; transgenic;  
 XX enzyme.  
 OS Homo sapiens.  
 XX WO2003033689-A1.  
 XX 24-APR-2003.  
 XX 12-OCT-2001; 2001WO-IB002407.  
 XX 12-OCT-2001; 2001WO-IB002407.  
 XX (CNRS ) CNRS CENT NAT RECH SCI.  
 XX Lazdunski M, Lambeau G, Valentin E;  
 XX WPI; 2003-403216/38.  
 XX Novel mammalian secreted group IIF secreted phospholipase A2, useful for  
 XX preventing and treating bacterial and viral infections, and cancers.  
 XX Disclosure; Fig 1; 33pp; English.  
 XX The invention relates to a mammalian secreted group IIF secreted  
 XX phospholipase A2 (sPLA2) (I), where the enzyme is Ca2+ dependent,  
 XX maximally active at pH 7-8 and hydrolyzes phosphatidylglycerol versus

phosphatidylcholine with a 15-fold preference. A pharmaceutical composition comprising (I) is useful for treating or preventing viral and bacterial infections, and cancers. A pharmaceutical composition containing compounds capable of inhibiting catalytic activity of (I), biologically active compounds that bind sPLA<sub>2</sub> receptors, or a compound that modulates cell proliferation, cell migration, cell contraction or apoptosis is useful for treating disease states or disorders involving group IIF sPLA<sub>2</sub>, such as inflammatory disease, cancers, cardiac and brain ischaemia, acute lung injury, acute respiratory distress syndrome or Crohn's disease. Specific antibodies are useful for searching new secreted mammalian group IIF sPLA<sub>2</sub> or the homologues of the enzyme in other mammals. The encoding polynucleotides and vectors are useful for transforming animals and establishing a line of transgenic animals. Sequences AB44232-238 represent various human secreted sPLA<sub>2</sub> enzymes used in alignment studies with the G1F sPLA<sub>2</sub> enzyme

XX Sequence 144 AA;

Query Match 45.1%; Score 368.5; DB 6; Length 144;  
Best Local Similarity 52.1%; Pred. No. 3.2e-26;  
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;  
QY 12 LLVALVT-----GNLVQGVMIKWTGK-SALQVNDYGCYCGIGGSHWPVDQTDWCC 62  
DB 5 LLLAVIMIFGLLOAHGNLVNFRHMIKLTGKEAALSIFYGCHGVGSGSPKDATDRCC 64  
QY 63 HAHDCCYGRLEKCEPKLEKYLFSVBERGIFCAGRTTCORLTCECDKRAALCFRRNLGT 122  
DB 65 VTHDCCYKRLKRGCGTKFLSYKFSNSGRITCAKQDSCRQSCDCAKAAATCFARNKTT 124  
QY 123 YNRKYAHVPNKLCTGTPPC 142  
DB 125 YNKYQYYSNKHCRGSTPRC 144

RESULT 12  
ABP96807  
ID ABP96807 standard; protein; 144 AA.

AC ABP96807;

XX 05-JUN-2003 (first entry)

XX Human phospholipase A2 group IIA (synovial) SEQ ID NO:3.

XX Phospholipase A2 group IIA; synovial; antisense modulation; inflammation;  
XX phospholipase A2 group IIA inhibitor; phosphorothioate; antiinflammatory;  
XX antidiabetic; cytostatic; antipsoriatic; vaccine; gene therapy; cancer;  
XX psoriasis; diabetes; enzyme.

XX Homo sapiens.

XX W0200297133-A1.

XX 05-DEC-2002.

XX 21-MAY-2002; 2002WO-US016135.

XX 25-MAY-2001; 2001US-00865866.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Wyatt JR;

XX WPI; 2003-140495/13.

XX N-PSDB; ACC46906, ACC46921.

XX New compound that hybridizes with and inhibits the expression of

PT Phospholipase A2, group IIA, useful for preparing a composition for

PT treating or preventing inflammation, cancer, psoriasis or diabetes.

XX Example 13; Page 95-96; 135pp; English.

CC The present invention describes a compound (I) comprising 8-50  
CC nucleobases which is targeted to a 5' untranslated region (UTR), coding,  
CC 3' UTR or intron region of a nucleic acid molecule encoding phospholipase  
CC A2, group IIA (synovial), where the compound specifically hybridizes with  
CC and inhibits the expression of phospholipase A2, group IIA (synovial).  
CC Also described: (1) a composition comprising the compound and a carrier  
CC or diluent; (2) a method of inhibiting the expression of phospholipase  
CC A2, group IIA in cells or tissues; and (3) a method of treating an animal  
CC having a disease or condition associated with phospholipase A2, group IIA  
CC (synovial). (1) has antiinflammatory, antidiabetic, cytostatic and  
CC antipsoriatic activities, and can be used in vaccines and in gene  
CC therapy. The compound (I) can be used for preparing a composition for  
CC treating or preventing inflammation, cancer, psoriasis or diabetes. The  
CC present sequence represents human phospholipase A2 group IIA (synovial),  
CC which is used in an example from the present invention

XX Sequence 144 AA;

Query Match 45.1%; Score 368.5; DB 6; Length 144;  
Best Local Similarity 52.1%; Pred. No. 3.2e-26;  
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;  
QY 12 LLVALVT-----GNLVQGVMIKWTGK-SALQVNDYGCYCGIGGSHWPVDQTDWCC 62  
DB 5 LLLAVIMIFGLLOAHGNLVNFRHMIKLTGKEAALSIFYGCHGVGSGSPKDATDRCC 64  
QY 63 HAHDCCYGRLEKCEPKLEKYLFSVBERGIFCAGRTTCORLTCECDKRAALCFRRNLGT 122  
DB 65 VTHDCCYKRLKRGCGTKFLSYKFSNSGRITCAKQDSCRQSCDCAKAAATCFARNKTT 124  
QY 123 YNRKYAHVPNKLCTGTPPC 142  
DB 125 YNKYQYYSNKHCRGSTPRC 144

RESULT 13  
ABU63123

ID ABU63123 standard; protein; 144 AA.

XX ABU63123;

XX 25-SEP-2003 (first entry)

XX Human group IIA secreted phospholipase A2.

XX Human; group IIA secreted phospholipase A2; virucide; antibacterial;  
XX cytostatic; antiinflammatory; vasotropic; cerebroprotective; sPLA<sub>2</sub>;  
XX phosphatidylglycerol hydrolysis; phosphatidylcholine hydrolysis;  
XX viral infection; bacterial infection; cancer; inflammatory disease;  
XX cardiac ischaemia; brain ischaemia; acute lung injury;  
XX acute respiratory distress syndrome; Crohn's disease; enzyme.

XX Homo sapiens.

XX US2003073087-A1.

XX 17-APR-2003.

XX 11-OCT-2001; 2001US-00975456.

XX 11-OCT-2000; 2000US-0239491P.

XX (LAZD/) LAZDUNSKI M.

XX (LAMB/) LAMBEAU G.

XX (VALE/) VALENTIN E.

XX Lazdunski M, Lambeau G, Valentin E;

XX WPI; 2003-567302/53.

XX New mammalian secreted group IIF phospholipase A2 or nucleic acid, useful  
PT for treating or preventing viral or bacterial infections, or cancers, or  
PT screening inhibitors of the enzyme for treating e.g. inflammatory



PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ - Sequence 144 AA;

Query Match 45.1%; Score 368.5; DB 7; Length 144;  
Best Local Similarity 52.1%; Pred. No. 3.2e-26;  
Matches 73; Conservative 12; Mismatches 46; Indels 9; Gaps 2;  
QY 12 LVALVT-----GNLVQFGVNIKMTGK-SALQNDYGYCGIGGSHWPVDQTDWCC 62  
Db 5 LLLAVINIFGLQAHGNLVNFRHMIKLTGKEAALSFGFYGCHGCVGGRGSPKDATDRCC 64  
QY 63 HAHDCCYGRLEKLCCEPKLEKYLFSYSESGIFCAGRTTCORLTCECDKRAALCFRNLGT 122  
Db 65 VTHDCCYKRLKRCGCGTKFLSYFNSGSRITCAKQDSQRSQLCEDCKAAATCFARNKTT 124  
QY 123 YNKYAHYPNKLCTGPTPPC 142  
Db 125 YNKKYQYYSNKHCRGSPRC 144

Search completed: July 3, 2004, 05:16:16  
Job time : 43.1887 secs





GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:14:29 ; Search time 10.6755 Seconds  
(without alignments)  
1108.294 Million cell updates/sec

Title: US-10-088-092A-30\_COPY\_20\_142

Perfect score: 722

Sequence: 1 NLVQFGVMIEKMTGKSAQY.....YNRKYAHYFNKLTGTPPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 781:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	372	51.5	121	2	S17860
2	360.5	49.9	144	1	PSHUFF
3	358.5	49.7	120	2	S13019
4	358	49.6	137	2	S22388
5	350	48.5	123	2	B53872
6	347	48.1	146	2	A33394
7	340	47.1	121	1	PSBGAC
8	339.5	47.0	122	1	PSYXAF
9	339.5	47.0	138	2	JC1342
10	337	46.7	146	2	A35493
11	335.5	46.5	138	2	I50098
12	335	46.4	146	2	I48342
13	333.5	46.2	122	2	A25806
14	333.5	46.2	138	2	S10333
15	333	46.1	146	2	JU0283
16	332.5	46.1	122	2	A33117
17	332.5	46.1	122	2	S33267
18	330.5	45.8	138	1	PSVIAA
19	330.5	45.8	138	1	PSVIAC
20	330.5	45.8	138	1	I51386
21	330	45.7	124	2	I51190
22	329.5	45.6	122	2	A44179
23	328.5	45.5	122	1	PSABA
24	326.5	45.2	138	2	S95522
25	325.5	45.1	121	2	S17861
26	325.5	45.1	138	2	F48188
27	324.5	44.9	122	2	A33972
28	324.5	44.9	122	2	A37478
29	324	44.9	145	2	I48093

## ALIGNMENTS

### RESULT 1

S17860

phospholipase A2 (EC 3.1.1.4) isoform A1 - leaf-nosed viper

C:Species: Eristocophis macmahoni (leaf-nosed viper)

C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 31-Oct-1997

C:Accession: S17860

R:Siddiqi, A.R.; Zaidi, Z.H.; Joernvall, H.

Eur. J. Biochem. 201, 675-679, 1991

A:Title: Purification and characterization of two highly different group II phospholipase A2

A:Reference number: S17860; MUID:92037623; PMID:1935962

A:Accession: S17860

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-121 <SID>

C:Superfamily: phospholipase A2

C:Keywords: carboxylic ester hydrolase

Query Match

Best Local Similarity 51.5%; Score 372; DB 2; Length 121;

Matches 70; Conservative 56.5%; Pred. NO. 5e-29;

Mismatches 8; Indels 4; Gaps 3;

QY	1	NLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGSGSHKPVDTWCCHAHDCCYGRLEKLGCE	59
Db	1	NLYQFGVMIFKMTGKSAALLSYDYCYGCGWKGKPLDTRCCFVHDCCYGRVN--GCN	58
QY	60	PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYFNKLTGTP	119
Db	59	PKLSTYSYSFQNGDIVCGDDNACLRAVCECDRVAICFGENLTYDRKYDYPSSQCT-E	117
QY	120	TPPC	123
Db	118	TEQC	121

### RESULT 2

PSHUYF

phospholipase A2 (EC 3.1.1.4) IIA precursor [validated] - human

N:Alternate names: phosphatidylcholine 2-acylhydrolase; placental pIA2; platelet-secreted

C:Species: Homo sapiens (man)

C:Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 15-Sep-2000

C:Accession: A32862; B32862; A60266; A32847; A60263; A31350; PT0056; A32913; A60265; A611

R:Kramer, R.M.; Hession, C.; Johansen, B.; Hayes, G.; McGray, P.; Chow, E.P.; Tizard, R.;

J. Biol. Chem. 264, 5768-5775, 1989

A:Title: Structure and properties of a human non-pancreatic phospholipase A-2.

A:Reference number: A32862; MUID:89174633; PMID:2925633

A:Accession: A32862

A:Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-144 <KRA>

A:Accession: B32862

A:Molecule type: protein

A:Residues: 21-39 <KR2>

A>Note: this protein was also detected in platelets  
 R:Kramer, R.M.; Johansen, B.; Hession, C.; Pepinsky, R.B.  
 Adv. Exp. Med. Biol. 275, 35-53, 1990  
 A>Title: Structure and properties of a secreted phospholipase A-2 from human platelets  
 A:Reference number: A60266; MUID:91050834; PMID:239446  
 A:Accession: A60266  
 A>Status: not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-144 <CRU>  
 R:Seilhamer, J.J.; Krzysanski, W.; Vadas, P.; Plant, S.; Miller, J.A.; Kloss, J.; Johnson  
 J. Biol. Chem. 264, 5335-5338, 1989  
 A>Title: Cloning and recombinant expression of phospholipase A-2 present in rheumatoid a  
 A:Reference number: A32847; MUID:89174566; PMID:2925608  
 A:Accession: A32847  
 A:Molecule type: mRNA  
 A:Residues: 1-144 <SKI>  
 A:Cross-references: GB:J04704; EMBL:M22430; NID:g190888; PID:AAA36550.1; PID:g190889  
 R:Crowl, R.; Stoner, C.; Stoller, T.; Pan, Y.C.; Conroy, R.  
 Adv. Exp. Med. Biol. 279, 173-184, 1990  
 A>Title: Isolation and characterization of cDNA clones from human placenta coding for ph  
 A:Reference number: A60263; MUID:91263879; PMID:1710870  
 A:Accession: A60263  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA  
 A:Residues: 1-144 <CRU>  
 R:Lai, C.Y.; Wada, K.  
 Biochem. Biophys. Res. Commun. 157, 488-493, 1988  
 A>Title: Phospholipase A-2 from human synovial fluid: purification and structural homolo  
 A:Reference number: A31350; MUID:89076274; PMID:3202859  
 A:Accession: A31350  
 A:Molecule type: protein  
 A:Residues: 21-33 <LAI>  
 R:Harai, S.; Kudo, I.; Matsura, K.; Miyamoto, T.; Inoue, K.  
 J. Biochem. 104, 326-328, 1988  
 A>Title: Amino acid composition and NH2-terminal amino acid sequence of human phospholip  
 A:Reference number: P70056; MUID:89197814; PMID:3240982  
 A:Accession: P70056  
 A:Molecule type: protein  
 A:Residues: 21-46, 'X', 48-54 <HAR>  
 R:Kanda, A.; Ono, T.; Yoshida, N.; Tojo, H.; Okamoto, M.  
 Biochem. Biophys. Res. Commun. 163, 42-48, 1989  
 A>Title: The primary structure of a membrane-associated phospholipase A-2 from human spl  
 A:Reference number: A32913; MUID:89374261; PMID:2775276  
 A:Accession: A32913  
 A:Molecule type: protein  
 A:Residues: 21-144 <KAN>  
 R:Parks, T.P.; Lukas, S.; Hoffman, A.F.  
 Adv. Exp. Med. Biol. 275, 55-81, 1990  
 A>Title: Purification and characterization of a phospholipase A-2 from human osteoarthri  
 A:Reference number: A60265; MUID:91050835; PMID:2146857  
 A:Accession: A60265  
 A:Molecule type: protein  
 A:Residues: 21-45, 'X', <PAR>  
 R:Recklies, A.D.; White, C.  
 Arthritis Rheum. 34, 1106-1115, 1991  
 A>Title: Phospholipase A-2 is a major component of the salt-extractable pool of matrix p  
 A:Reference number: A61201; MUID:92029121; PMID:1930329  
 A:Accession: A61201  
 A:Molecule type: protein  
 A:Residues: 21-40 <REC>  
 R:Green, J.A.; Smith, G.M.; Buchta, R.; Lee, R.; Ho, K.Y.; Rajkovic, I.A.; Scott, K.F.  
 Inflammation 15, 355-366, 1991  
 A>Title: Circulating phospholipase A-2 activity associated with sepsis and septic shock  
 A:Reference number: A61634; MUID:92098137; PMID:1757123  
 A:Accession: A61634  
 A:Molecule type: protein  
 A:Residues: 21-44 <GRE>  
 R:Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods  
 Teater, C.; Warrick, M.W.; Jones, N.D.  
 submitted to the Brookhaven Protein Data Bank, May 1992  
 A:Reference number: A51043; PDB:1BBC  
 A:Contents: annotation; X-ray crystallography, 2.2 angstroms, residues 21-144

R:Wery, J.P.; Schevitz, R.W.; Clawson, D.K.; Bobbitt, J.L.; Dow, E.R.; Gamboa, G.; Goods  
 Teater, C.; Warrick, M.W.; Jones, N.D.  
 Nature 352, 79-82, 1991  
 A>Title: Structure of recombinant human rheumatoid arthritic synovial fluid phospholipase  
 A:Reference number: A58514; MUID:91287826; PMID:2062381  
 A:Contents: annotation; X-ray crystallography  
 C:Genetics: PLA2G2A; PLA2B; PLA2L  
 A:Gene: GDB:PLA2G2A; PLA2B; PLA2L  
 A:Cross-references: GDB:120296; OMIM:172411  
 A:Map position: lp36.1-1p35  
 A:Introns: 14/1; 62/2; 98/1  
 C:Function:  
 A:Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-  
 A>Note: the reaction is strongly enhanced when the phospholipid is condensed into a micel  
 C:Superfamily: phospholipase A2  
 C:Keywords: calcium; carboxylic ester hydrolase; extracellular protein; lipid degradatio  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-144/Product: phospholipase A2 IIA #status experimental <MAT>  
 F:46-137/48-64, 63-117, 69-144, 70-110, 79-103, 97-108/disulfide bonds: #status experimental  
 F:47, 49, 51, 68/Binding site: calcium (His, Gly, Asp) #status predicted  
 F:67, 111/Active site: His, Asp #status predicted  
 Query Match 49.9%; Score 360.5; DB 1; Length 144;  
 Best Local Similarity 55.6%; Pred. No. 7.6e-28;  
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;  
 QY 1 NLVQFGVMIEKMTGK-SALQYNDYCYGICGGSHWPDQTDWCCHADCCYGRLEKLGCE 59  
 Db 21 NLVNFHRIKLTGKEALSFGYCHGCVGRSPKDATDCCVTHDCCYKLEKRGCG 80  
 QY 60 PKLEKYLFSVSRGIFCAGRTTCORLTCECDKRALCFRNLTGYNRYAHYHNKLTGTP 119  
 Db 81 TKFLSYKTSNLSGRITCAKQDSRSQLCECDKAAATCFARNKTTYNNKYQYYSNKHCRGS 140  
 QY 120 TPQC 123  
 Db 141 TPRC 144  
 RESULT 3  
 S13019  
 Phospholipase A2 (EC 3.1.1.4) - horn viper  
 C:Species: Cerastes cerastes (horn viper)  
 C>Date: 19-Mar-1997 #sequence revision 19-Mar-1997 #text\_change 31-Oct-1997  
 C:Accession: S13019  
 R:Siddiqi, A.R.; Shafiqat, J.; Zaidi, Z.H.; Joernvall, H.  
 FEBS Lett. 278, 14-16, 1991  
 A>Title: Characterization of phospholipase A2 from the venom of Horned viper (Cerastes ca  
 A:Reference number: S13019; MUID:91130587; PMID:1993470  
 A:Accession: S13019  
 A>Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 1-120 <SID>  
 C:Superfamily: phospholipase A2  
 C:Keywords: carboxylic ester hydrolase  
 Query Match 49.7%; Score 358.5; DB 2; Length 120;  
 Best Local Similarity 54.2%; Pred. No. 1e-27;  
 Matches 64; Conservative 10; Mismatches 41; Indels 3; Gaps 2;  
 QY 1 NLVQFGVMIEKMTGKSAI-QYNDYCYGICGGSHWPDQTDWCCHADCCYGRLEKLGCE 59  
 Db 1 NLVQFGVMIFKMTGKSPFISYGDYCYCGWGGKGTVDATDRCDFVHDCCYGRVN--SCN 58  
 QY 60 PKLEKYLFSVSRGIFCAGRTTCORLTCECDKRALCFRNLTGYNRYAHYHNKLTCT 117  
 Db 59 PKRSTYSYFQNGIVGDDQNLCKRAVCECDRAAICFGENVNTYDKKYKDYPTSQCT 116  
 RESULT 4  
 S22388  
 Phospholipase A2 (EC 3.1.1.4) amodytin I2 precursor - western sand viper  
 C:Species: Vipera ammodytes ammodytes (western sand viper)

Dd    1 NLFQFEKLKIQVTKSGMLWYSAYGCVGMGGQRPKDATDRCCFVHDDCYGVK--TGCN 58

Qy    60 PLEKYLVSVSERGIFCAGRITTCORLTCECDKRALCFRNGLGTYNRK-YAHYPNKLCCTG 118  
       |::|::||                |::|::||                |:  
Dd    59 PRWDIVTSVDNGNVCGGTNPCKKQCICEDRAAIAFRDLNLTYDSKTWKYPKNCKE 118  
       |::|::||                |::|::||                |:  
Qy    119 PTTPC 123  
       ||  
Dd    119 ESEPC 123  
       :||

RESULT 6

A33394

phospholipase A2 (EC 3.1.1.4) precursor (version 1) - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 29-Jan-1990 #sequence\_revision 29-Jan-1990 #text\_change 20-Jun-2000

C/Acession: A33394; JU0131

R/Ichizaki, J.; Ohara, O.; Nakamura, E.; Tanaka, M.; Ono, T.; Kanda, A.; Yoshida, H.

Biochem. Biophys. Res. Commun. 162, 1030-1036, 1989

A>Title: cDNA cloning and sequence determination of rat membrane-associated phospholipase A2

A/Reference number: A33394; PMID:89350908; PMID:2764915

A/Acession: A33394

A>Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-146 <ISH>

A/Cross-references: GB:M25148

P/Komada, M.; Kudoh, I.; Mizushima, H.; Kitamura, N.; Inoue, K.

J. Biochem. 106, 545-547, 1989

A>Title: Structure of cDNA coding for rat platelet phospholipase A2.

A/Reference number: JU0131; PMID:90110043; PMID:2606907

A/Acession: JU0131

A/Molecule type: mRNA

A/Residues: 1-146 <KOM>

A/Cross-references: GB:D00523; NID:g220857; PIDN:BAA00410.1; PID:g220858

C/Superfamily: phospholipase A2

C/Keywords: carboxylic ester hydrolase

F/1-21/Domain: signal sequence #status predicted <SIG>

F/22-146/Product: phospholipase A2 #status predicted <MAT>

F/69,113/Active site: His, Asp #status predicted

Query Match      48.1%; Score 347; DB 2; Length 146;  
Best Local Similarity    51.2%; Pred. No. 1.6e-26;  
Matches    64; Conservative    14; Mismatches    45; Indels    2; Gaps    2

Qy    1 NLVFQGWTEIKMTKGSA-LQYNDYGVCYGGSHWPVDQDWCHACHDCYCGRLEKLGC 59  
       |::|::||                |::|::||                |:  
Dd    22 SLLFGQMILFTKTRADVSIFYGYGHVGGRSPKDATTWCVTHTDCCVNLELRKGC 81  
       |::|::||                |::|::||                |:

Qy    60 PLEYLVSVERGIFFCA-GRTTCORTCBCEDKRALCLPRNLGTYNRKAHYPNKLCCTG 118  
       |::|::||                |::|::||                |:  
Dd    82 TKFLTYKFSYRGQGISCSTNQDSPCRQLQQCDRAAAEFARNKKSLYQFYFNPFCKG 141  
       |::|::||                |::|::||                |:

Qy    119 PTTPC 123  
       ||  
Dd    142 KTPSC 146  
       |||

RESULT 7

PSBGAC

phospholipase A2 (EC 3.1.1.4) - horned viper

N/Alternate names: caudoxin ; phosphatidylcholine 2-acetylhydrolase

C/Species: Bitis caudalis (horned viper)

C/Date: 17-Dec-1982 #sequence\_revision 17-Dec-1982 #text\_change 24-Apr-1998

C/Acession: A00762

R/Viljoen, C.C.; Botes, D.P.; Kruger, H.  
Toxicol 20, 715-737, 1982

A>Title: Isolation and amino acid sequence of caudoxin, a presynaptic acting toxin

A/Reference number: A00762; PMID:83042262; PMID:7135414

A/Acession: A00762

A/Molecule type: protein

A/Residues: 1-121 <VII>

C/Comment: This enzyme is a presynaptic neurotoxin.

C/Function:

A;Description: catalyzes hydrolysis of 1,2-diacyl-sn-glycero-3-phosphocholine to 1-acyl-  
 A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle  
 C;Superfamily: phospholipase A2  
 C;Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres  
 F:25-121,27-43,42-94,48-114,49-87,56-80,74-85/Disulfide bonds: #status predicted  
 F:26,28,30,47/Binding site: calcium (Tyr, Gly, Asp) #status predicted  
 F:46,68/Active site: His, Asp #status predicted

Query Match 47.1%; Score 340; DB 1; Length 121;  
 Best Local Similarity 47.2%; Pred. No. 6.3e-26;  
 Matches 58; Conservative 15; Mismatches 48; Indels 2; Gaps 1;  
 QY 1 NLVQFGVMIEKMTGKSAIQNDYCYGCGIGGSHWVPDQTCWCHADCCYGRLEKLGCEP 60  
 DB 1 NLIQFGNMISATGKSSLAYASYGCGWGGKQPKDDTRCCFVHDCCYGKADK--CSP 58  
 QY 61 KLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLTCTGPT 120  
 DB 59 KMILYSYKFNHNGIVCGDKNAKKVCECDRAAICFAASGHSYKNLWYPPSSKCTGTA 118  
 QY 121 PPC 123  
 DB 119 EKC 121

## RESULT 8

Phospholipase A2 (EC 3.1.1.4) X - habu  
 N;Alternate names: phosphatidylcholine 2-acylhydrolase  
 C;Species: Trimeresurus flavoviridis (habu)  
 C;Date: 30-Sep-1987 #sequence\_revision 30-Sep-1987 #text\_change 24-Apr-1998  
 C;Accession: A25500  
 R;Kinul, R.M.; Kawabata, S.I.; Iwanaga, S.  
 A;Title: Comparison of amino terminal region of three isoenzymes of phospholipases A2 (T  
 A;Note: the reaction is strongly enhanced when the phospholipid is condensed into a micelle  
 C;Superfamily: phospholipase A2  
 C;Keywords: calcium; carboxylic ester hydrolase; homodimer; lipid degradation; metallopro  
 F:26-122,28-44,43-95,49-115,50-88,57-81,75-86/Disulfide bonds: #status predicted  
 F:27,29,31,48/Binding site: calcium (Tyr, Gly, Asp) #status predicted  
 F:47,89/Active site: His, Asp #status predicted

Query Match 47.0%; Score 339.5; DB 1; Length 122;  
 Best Local Similarity 49.2%; Pred. No. 7.1e-26;  
 Matches 61; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKMTGKSAIQNDYCYGCGIGGSHWVPDQTCWCHADCCYGRLEKLGCE 59  
 DB 1 HLLQFRMKIKMTGKEPIVSFAFYCYGCGGGRGKPKDADTRCCFVHDCCYEKV--TGCD 58  
 QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLTCTGP 119  
 DB 59 PKWSYTYTSLNGDIVCGDPVCTKVKCECDKAAICFRDNLKTYKNRYMTFPDICTDP 118

QY 120 TPPC 123

DB 119 TEGC 122

## RESULT 9

Phospholipase A2 (EC 3.1.1.4) precursor - halys viper  
 C;Species: Agkistrodon halys (halys viper)  
 C;Date: 09-Oct-1997 #sequence\_revision 07-Nov-1997 #text\_change 13-Nov-1998  
 C;Accession: JCI1342  
 R;Pan, H.; Ou-Yang, L.L.; Yang, G.Z.; Zhou, Y.C.; Wu, X.F.

Acta Biochim. Biophys. Sin. 28, 579-582, 1996

A;Title: Cloning of the bPLA2 gene from Agkistrodon halys Pallas.

A;Reference number: JCI1342

A;Contents: Snake venom

A;Accession: JCI1342

A;Molecule type: mRNA

A;Residues: 1-138 <PAN>

A;Note: the authors translated the codon GAC for residue 54 as Asn

C;Comment: This protein catalyzes specifically the hydrolysis of the C-2 ester bond of 3-

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

F:1-15/Domain: signal sequence #status predicted <SIG>

F:17-138/Product: phospholipase A2 #status predicted <MAT>

Query Match 47.0%; Score 339.5; DB 2; Length 138;  
 Best Local Similarity 50.0%; Pred. No. 7.9e-26;  
 Matches 62; Conservative 15; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKMTGKS-ALQNDYCYGCGIGGSHWVPDQTCWCHADCCYGRLEKLGCE 59  
 DB 17 SLIQFRMKIKMTGKEPVVSFAFYCYGCGGGRGKPKDADTRCCFVHDCCYEKL--TGCD 74

QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLTCTGP 119  
 DB 75 PKWDDYTYSWKNGTIVCGDDPCKEKEVCECDKAAICFRDNLKTYKNRYMTYPNLCSSK 134

QY 120 TPPC 123

DB 135 SEKC 138

## RESULT 10

A35493

Phospholipase A2 (EC 3.1.1.4) II precursor - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 14-Sep-1990 #sequence\_revision 18-Nov-1992 #text\_change 18-Jun-1999

C;Accession: A35493; S11388; S71310

R;Komada, M.; Kudo, I.; Inoue, K.

Biochem. Biophys. Res. Commun. 168, 1059-1065, 1990

A;Title: Structure of gene coding for rat group II phospholipase A-2.

A;Reference number: A35493; MUID:90267443; PMID:2346480

A;Accession: A35493

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-146 <KOM>

A;Cross-references: GB:M37127; NID:G204318; PIDN:AAA41223.1; PID:G204319

A;Note: the authors translated the codon TAT for residue 42 as Thr

R;Kusunoki, C.; Satoh, S.; Kobayashi, M.; Niwa, M.

Biochim. Biophys. Acta 1087, 95-97, 1990

A;Title: Structure of genomic DNA for rat platelet phospholipase A(2).

A;Reference number: S11388; MUID:90381322; PMID:2400792

A;Accession: S11388

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-146 <KUS>

A;Cross-references: EMBL:X51529; NID:G56930; PIDN:CAA35909.1; PID:G56931

R;Aarsman, A.J.; Schaakwijk, C.G.; Neys, F.W.; Iijima, N.; Wherrett, J.R.; van den Bosch,

Arch. Biochem. Biophys. 331, 95-103, 1996

A;Title: Purification and characterization of Ca(2+)-dependent phospholipases A(2) from :

A;Reference number: S71310; MUID:96268465; PMID:8660688

A;Accession: S71310

A;Molecule type: protein

A;Residues: 22-29, X', 31-32, X', 34 <AAP>

A;Experimental source: kidney

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase; lipid degradation

F:68,113/Active site: His, Asp #status predicted

Query Match 46.7%; Score 337; DB 2; Length 146;

Best Local Similarity 50.4%; Pred. No. 1.4e-25;

Matches 63; Conservative 14; Mismatches 46; Indels 2; Gaps 2;

QY 1 NLVQFGVMIEKMTGKSA-LQNDYCYGCGIGGSHWVPDQTCWCHADCCYGRLEKLGCE 59

```
submitted to the EMBL Data Library, July 1993
A:Reference number: S35948
A:Accession: S35948
A:Molecule type: mRNA
A:Residues: 22-115, 'R', 118-146 <MUL3>
A:Cross-references: EMBL:X74266
J.Kennedy, B.P.; Pavette, P.; Mudgett, J.; Vadas, P.; Pruzanski, W.; Kwan, M.; Tang, C.;
J. Biol. Chem. 270, 22378-22385, 1995
A:Title: A natural disruption of the secretory group II phospholipase A2 gene in inbred n
A:Reference number: I49352; MUID:95403435; PMID:1673223
A:Accession: I49352
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-18, 'V', 20-85, 'K', 87-146 <KEN>
A:Cross-references: EMBL:U32358; NID:G984836; PIDN:AAC52252.1; PID:G984837
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:68,113/Active site: His, Asp #status predicted

Query Match 46.4%; Score 335; DB 2; Length 146;
Best Local Similarity 52.0%; Pred. No. 2.3e-25;
Matches 65; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 1 NLVQFGVMIEKWTGKSA-LQYNDYCYGCGGGSHWPVDQTDWCCHAHDCGGRLEKLGCE 59
DB 22 NIAQFGEMIRLTKGRBELSYAFYGCGLGKSPKDATDRCCVTHDCCYKSLKSGCG 81
QY 60 PKLEYLFSVBERGIFC-AGRTTCORLTCECDKRAALCFRNLTGTYNRKYAHYPNKLCTGP 118
DB 82 TKLLTYKYSHOGGQITCSANQNSCKRLCQCDKAAAECAFARKKTYSLKYQFYFNMFCG 141
QY 119 TTPPC 123
DB 142 KXPKC 146

RESULT 13
phospholipase A2 (EC 3.1.1.4) B - western sand viper
N:Alternate names: amodytoxin B
C:Species: Viper amodytes amodytes (western sand viper)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 28-Aug-1998
C:Accession: A25806
R:Ritonja, A.; Machleidt, W.; Turk, V.; Gubensek, F.
Biol. Chem. Hoppe-Seyler 367, 919-923, 1986
A:Title: Amino-acid sequence of amodytoxin B partially reveals the location of the site
A:Reference number: A25806; MUID:87076055; PMID:3790259
A:Accession: A25806
A:Molecule type: protein
A:Residues: 1-122 <RIT>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:26-115,28-44,43-95,49-122,50-88,57-81,75-86/Disulfide bonds: #status predicted
F:47,89/Active site: His, Asp #status predicted

Query Match 46.2%; Score 333.5; DB 2; Length 122;
Best Local Similarity 47.6%; Pred. No. 2.7e-25;
Matches 59; Conservative 18; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKWTGKSA-LQYNDYCYGCGGGSHWPVDQTDWCCHAHDCGGRLEKLGCE 59
DB 1 SILLEFGMILGETGKNPLTSYFYGCYGVGGKGTPKDATDRCCFVHDCCYGNLP--DCS 58
QY 60 PKLEYLFSVBERGIFCAGRTTCORLTCECDKRAALCFRNLTGTYNRKYAHYPNKLCTGP 119
DB 59 PKTDRYKTHRENGAIVCGKTSNCEICEDRAAAICFRKLNKTYNHIYMYIPDFLCKE 118
QY 120 TTPC 123
DB 119 SEKC 122

RESULT 14
phospholipase A2 (EC 3.1.1.4), secretory group II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48342; PC2009; S35948; I49352
R:Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A:Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines: F
A:Reference number: I48342; MUID:94029955; PMID:8267757
A:Accession: I48342
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-146 <MUL1>
A:Cross-references: EMBL:X74266; NID:G557247; PIDN:CAA52325.1; PID:G557248
R:Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1993
A:Title: Enhancing factor, a paneth cell specific protein from mouse small intestines: F
A:Reference number: PC2009; MUID:94071967; PMID:8250944
A:Accession: PC2009
A:Molecule type: mRNA
A:Residues: 22-146 <MUL2>
A:Note: correction of S35948
R:Mulherkar, R.; Rao, R.; Wagle, A.; Patki, V.; Deo, M.
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submitted to the EMBL Data Library, July 1993
A:Reference number: S35948
A:Accession: S35948
A:Molecule type: mRNA
A:Residues: 22-115, 'R', 118-146 <MUL3>
A:Cross-references: EMBL:X74266
J.Kennedy, B.P.; Pavette, P.; Mudgett, J.; Vadas, P.; Pruzanski, W.; Kwan, M.; Tang, C.;
J. Biol. Chem. 270, 22378-22385, 1995
A:Title: A natural disruption of the secretory group II phospholipase A2 gene in inbred n
A:Reference number: I49352; MUID:95403435; PMID:1673223
A:Accession: I49352
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 1-18, 'V', 20-85, 'K', 87-146 <KEN>
A:Cross-references: EMBL:U32358; NID:G984836; PIDN:AAC52252.1; PID:G984837
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:68,113/Active site: His, Asp #status predicted

Query Match 46.4%; Score 335; DB 2; Length 146;
Best Local Similarity 52.0%; Pred. No. 2.3e-25;
Matches 65; Conservative 9; Mismatches 49; Indels 2; Gaps 2;

QY 1 NLVQFGVMIEKWTGKSA-LQYNDYCYGCGGGSHWPVDQTDWCCHAHDCGGRLEKLGCE 59
DB 22 NIAQFGEMIRLTKGRBELSYAFYGCGLGKSPKDATDRCCVTHDCCYKSLKSGCG 81
QY 60 PKLEYLFSVBERGIFC-AGRTTCORLTCECDKRAALCFRNLTGTYNRKYAHYPNKLCTGP 118
DB 82 TKLLTYKYSHOGGQITCSANQNSCKRLCQCDKAAAECAFARKKTYSLKYQFYFNMFCG 141
QY 119 TTPPC 123
DB 142 KXPKC 146

RESULT 13
phospholipase A2 (EC 3.1.1.4) B - western sand viper
N:Alternate names: amodytoxin B
C:Species: Viper amodytes amodytes (western sand viper)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 28-Aug-1998
C:Accession: A25806
R:Ritonja, A.; Machleidt, W.; Turk, V.; Gubensek, F.
Biol. Chem. Hoppe-Seyler 367, 919-923, 1986
A:Title: Amino-acid sequence of amodytoxin B partially reveals the location of the site
A:Reference number: A25806; MUID:87076055; PMID:3790259
A:Accession: A25806
A:Molecule type: protein
A:Residues: 1-122 <RIT>
C:Superfamily: phospholipase A2
C:Keywords: carboxylic ester hydrolase
F:26-115,28-44,43-95,49-122,50-88,57-81,75-86/Disulfide bonds: #status predicted
F:47,89/Active site: His, Asp #status predicted

Query Match 46.2%; Score 333.5; DB 2; Length 122;
Best Local Similarity 47.6%; Pred. No. 2.7e-25;
Matches 59; Conservative 18; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQFGVMIEKWTGKSA-LQYNDYCYGCGGGSHWPVDQTDWCCHAHDCGGRLEKLGCE 59
DB 1 SILLEFGMILGETGKNPLTSYFYGCYGVGGKGTPKDATDRCCFVHDCCYGNLP--DCS 58
QY 60 PKLEYLFSVBERGIFCAGRTTCORLTCECDKRAALCFRNLTGTYNRKYAHYPNKLCTGP 119
DB 59 PKTDRYKTHRENGAIVCGKTSNCEICEDRAAAICFRKLNKTYNHIYMYIPDFLCKE 118
QY 120 TTPC 123
DB 119 SEKC 122

RESULT 14
phospholipase A2 (EC 3.1.1.4), secretory group II - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 18-Jun-1999
C:Accession: I48342; PC2009; S35948; I49352
R:Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 195, 1254-1263, 1993
A:Title: Enhancing factor, a Paneth cell specific protein from mouse small intestines: F
A:Reference number: I48342; MUID:94029955; PMID:8267757
A:Accession: I48342
A:Status: preliminary; translated from GB/EMBL/DBD
A:Molecule type: mRNA
A:Residues: 1-146 <MUL1>
A:Cross-references: EMBL:X74266; NID:G557247; PIDN:CAA52325.1; PID:G557248
R:Mulherkar, R.; Rao, R.S.; Wagle, A.S.; Patki, V.; Deo, M.G.
Biochem. Biophys. Res. Commun. 197, 351-352, 1993
A:Title: Enhancing factor, a paneth cell specific protein from mouse small intestines: F
A:Reference number: PC2009; MUID:94071967; PMID:8250944
A:Accession: PC2009
A:Molecule type: mRNA
A:Residues: 22-146 <MUL2>
A:Note: correction of S35948
R:Mulherkar, R.; Rao, R.; Wagle, A.; Patki, V.; Deo, M.
```

S10333  
ammodytoxin B precursor - sand viper  
C:Species: Vipera ammodytes (sand viper)  
C:Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 18-Jun-1999  
C:Accession: S10333  
F:Kordis, D.; Pungercar, J.; Strukelj, B.; Liang, N.; Gubensek, F.  
Nucleic Acids Res. 18, 4016, 1990  
A:Title: Sequence of the cDNA coding for ammodytoxin B.  
A:Reference number: S10333; MUID:90326552; PMID:2374735  
A:Accession: S10333  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-138 <KOR>  
A:Cross-references: EMBL:X52241; NID:964441; PIDN:CAA36486.1; PID:964442  
C:Superfamily: phospholipase A2

Query Match 46.2%; Score 333.5; DB 2; Length 138;  
Best Local Similarity 47.6%; Pred. No. 3e-25; Gaps 2;  
Matches 59; Conservative 18; Mismatches 44; Indels 3; Gaps 2;  
Qy 1 NLVQGVMIERTGKSAI-QYNDYGCYGGSHWPVDQTDWCHADCCYGRLEKLGCE 59  
Db 17 SLLEFGMILGETGKPLTYSFYGCYGVGKGTGPKDATDRCCFVHDCCYGNLP--DCS 74  
Qy 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCEDKRAALCFRNLGTYNRYKHYHYPNKLCTGP 119  
Db 75 PKTRYKHYHRENGAIVCGKGTSCENRICECDRAAAICFRKNLKTNYHIYMYDFLCKKE 134  
Qy 120 TPPC 123  
Db 135 SEKC 138

RESULT 15  
JU0283  
phospholipase A2 (EC 3.1.1.4) precursor (version 2) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 07-Sep-1990 #sequence\_revision 07-Sep-1990 #text\_change 24-Jul-1997  
C:Accession: JU0283  
R:Komada, M.; Kudo, I.; Mizushima, H.; Kitamura, N.; Inoue, K.  
J. Biochem. 106, 545-547, 1989  
A:Title: Structure of cDNA coding for rat platelet phospholipase A2.  
A:Reference number: JU0131; MUID:90110043; PMID:2606907  
A:Accession: JU0283  
A:Molecule type: mRNA  
A:Residues: 1-146 <KOM>  
C:Superfamily: phospholipase A2  
C:Keywords: carboxylic ester hydrolase  
F:1-21/Domain: signal sequence #status predicted <SIG>  
F:22-146/Product: phospholipase A2 #status predicted <MAT>  
F:68,113/Active site: His, Asp #status predicted

Query Match 46.1%; Score 333; DB 2; Length 146;  
Best Local Similarity 49.6%; Pred. No. 3.5e-25; Gaps 2;  
Matches 62; Conservative 14; Mismatches 47; Indels 2; Gaps 2;  
Qy 1 NLVQGVMIERTGKSAI-QYNDYGCYGGSHWPVDQTDWCHADCCYGRLEKLGCE 59  
Db 22 SLLEFGMILFKTKRADVSYGFYGCYGVGGRSPKDATDWCCVTHGCCYNLLEKRGCG 81  
Qy 60 PKLEKYLFSVSRGIFCA-GTTTCQRLTCEDKRAALCFRNLGTYNRYKHYHYPNKLCTG 118  
Db 82 TKFTYKFSYRGQISCSSTNODSCRKQLCCDKAAAECAFARNKKSYSLKRYQFIPNFKCKG 141  
Qy 119 TPPC 123  
Db 142 KTPSC 146

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:12:38 ; Search time 8.81897 Seconds  
(without alignments)  
726.242 Million cell updates/sec

Title: US-10-088-092a-30\_COPY\_20\_142

Perfect score: 722

Sequence: 1 NLVQFGVMIKMTGKSALQY.....YNEKYAHYPNKLTGTPTPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	722	100.0	142	1 PA2E HUMAN	Q9NZK7 homo sapien
2	662	91.7	142	1 PA2E MOUSE	Q9GUL3 mus musculu
3	372	51.5	121	1 PA21_ERIMA	P24393 eristocophi
4	360.5	49.9	144	1 PA2A_HUMAN	P14555 homo sapien
5	358.5	49.7	120	1 PA2 CERCE	P21789 cerastes ce
6	358	49.6	137	1 PA2N VIPAA	P34180 vipera ammo
7	355	49.2	121	1 PA2 DABRR	P81458 daboia russ
8	350	48.5	123	1 PA21 AGKPI	P51972 agkistrodon
9	347	48.1	146	1 PA2A RAT	P14423 rattus norv
10	344.5	47.7	138	1 PA2Q TRIFL	Q8J190 trimeresuru
11	344.5	47.7	138	1 PA2Y TRIFL	Q90Y77 trimeresuru
12	341	47.2	146	1 PA2A MOUSE	P31482 mus musculu
13	340.5	47.2	122	1 PA2A TRIFL	P59264 trimeresuru
14	340	47.1	121	1 PA2 BITCA	P00622 bitis cauda
15	339.5	47.0	122	1 PA2X TRIFL	P06860 trimeresuru
16	339.5	47.0	138	1 PA2A AGKHP	Q42187 agkistrodon
17	339	47.0	137	1 PA2B VIPPA	Q3Y9J7 vipera pala
18	338.5	46.9	122	1 PA29 AGKHP	Q42188 agkistrodon
19	338.5	46.9	122	1 PA2B TRIFL	P59265 trimeresuru
20	337.5	46.7	138	1 PA2W TRIFL	Q02517 trimeresuru
21	335.5	46.5	138	1 PA21 BOTJR	P45881 bothrops ja
22	334.5	46.3	138	1 PA2B TRIGA	P70088 trimeresuru
23	333.5	46.2	138	1 PA2B VIPAA	P14424 vipera ammo
24	332.5	46.1	121	1 PA2B DABRR	P59071 daboia russ
25	332.5	46.1	122	1 PA2 AGKHA	P20249 agkistrodon
26	332.5	46.1	122	1 PA2 VIPBB	P31854 vipera beru
27	330.5	45.8	138	1 PA2A VIPAA	P10427 vipera ammo
28	330.5	45.8	138	1 PA2C VIPAA	P11407 vipera ammo
29	329.5	45.6	122	1 PA22 TRIGA	P81478 trimeresuru
30	328.5	45.5	122	1 PA21 AGKHA	P04417 agkistrodon
31	327.5	45.4	138	1 PA2 TRIGU	Q8J1Y9 trimeresuru
32	326.5	45.2	138	1 PA22 TRIMU	Q91968 trimeresuru
33	326.5	45.2	138	1 PA2A TRIMU	Q90W39 trimeresuru

34	325.5	45.1	121	1 PA22_ERIMA	P24294 eristocophi
35	325.5	45.1	122	1 PA28 AGKHP	Q42192 agkistrodon
36	325.5	45.1	138	1 PA2P TRIFL	Q92147 trimeresuru
37	324.5	44.9	122	1 PA23 TRIGA	P81480 trimeresuru
38	324.5	44.9	138	1 PA25 ECHOC	P59171 echis ocell
39	324	44.9	124	1 PA26 AGKHP	O42190 agkistrodon
40	324	44.9	145	1 PA2M_CAVPO	P47711 cavia porce
41	321.5	44.5	122	1 PA23 AGKHP	P14421 agkistrodon
42	320.5	44.4	122	1 PA21 TRIMU	Q91506 trimeresuru
43	319.5	44.3	138	1 PA21 TRIGA	P20476 trimeresuru
44	319.5	44.3	138	1 PA2A CROSS	P18998 crotalus sc
45	318.5	44.1	122	1 PA21_BOTAS	P20474 bothrops as

#### ALIGNMENTS

RESULT 1  
PA2E HUMAN STANDARD; PRT; 142 AA.  
AC Q9NZK7  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)  
DE (Phosphatidylcholine 2-acylhydrolase GIIE) (GIIE SPLA2) (SPLA(2)-IIE).  
GN PLA2G2E.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RX MEDLINE=2014788; PubMed=10681567;  
RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,  
RA Fujii N., Kawamoto K., Hanasaki K.;  
RT "Structures, enzymatic properties, and expression of novel human and  
mouse secretory phospholipase A(2)s.";  
RL J. Biol. Chem. 275:5785-5793(2000).  
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
acyl groups in 3-sn-phosphoglycerides. Has a preference for  
arachidonic-containing phospholipids.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
acylglycerophosphocholine + a fatty acid anion.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Restricted to the brain, heart, lung, and  
placenta.  
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
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EMBL; AF189279; AAF36541.1; -.  
HSSP; P14555; 1POD.  
GO; GO:0004624; F:secreted phospholipase A2 activity; TAS.  
GO; GO:0006954; P:inflammatory response; TAS.  
GO; GO:0006644; P:phospholipid metabolism; TAS.  
InterPro; IPR001211; PhospholipaseA2.  
Pfam; PF00068; Phoslip; 1.  
PRINTS; PR00389; PHPLIPASEA2.  
ProDom; PD000303; PhospholipaseA2; 1.  
SMART; SM00085; PA2c; 1.  
PROSITE; PS00119; PA2 ASP; FALSE\_NEG.  
PROSITE; PS00118; PA2\_HIS; 1.  
KW Hydrolase; Lipid degradation; Signal; Calcium.  
FT SIGNAL 1 19 POTENTIAL.  
FT CHAIN 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.

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FT ACT SITE 65 65 BY SIMILARITY.
FT ACT SITE 109 109 BY SIMILARITY.
FT DISULFID 44 135 BY SIMILARITY.
FT DISULFID 46 62 BY SIMILARITY.
FT DISULFID 61 115 BY SIMILARITY.
FT DISULFID 67 142 BY SIMILARITY.
FT DISULFID 68 108 BY SIMILARITY.
FT DISULFID 77 101 BY SIMILARITY.
FT DISULFID 95 106 BY SIMILARITY.
FT METAL 45 45 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 49 49 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 66 66 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 142 AA; 15989 MW; 3C360EA710E141FB CRC64;

Query Match 100.0%; Score 722; DB 1; Length 142;
Best Local Similarity 100.0%; Pred No. 5.4e-71; Indels 0; Gaps 0;
Matches 123; Conservative 0; Mismatches 0;

QY 1 NLVFGVMIERTGKSAQYNDYCYCGIGGSHWVPDQTDWCHAHDCCYGRLEKLGCEP 60
DB 20 NLVFGVMIERTGKSAQYNDYCYCGIGGSHWVPDQTDWCHAHDCCYGRLEKLGCEP 79
QY 61 KLEKYLFSVSEGIIFCAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHYPNKLTGTPT 120
DB 80 KLEKYLFSVSEGIIFCAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHYPNKLTGTPT 139
QY 121 PPC 123
DB 140 PPC 142

RESULT 2
PAZE MOUSE
ID PAZE MOUSE STANDARD; PRT; 142 AA.
AC Q9QUL3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Group IIE secretory phospholipase A2 precursor (EC 3.1.1.4)
DE (Phosphatidylcholine 2-acylhydrolase G1IE) (G1IE sPLA2) (sPLA(2)-IIE).
GN PLA2G2B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20002639; PubMed=10531313;
RA Valentin E., Ghomashchi F., Gelb M.H., Lazdunski M., Lambeau G.;
RT "On the diversity of secreted phospholipases A2. Cloning, tissue
RT distribution, and functional expression of two novel mouse group II
RT enzymes."
RL J. Biol. Chem. 274:31195-31202(1999).
RN [2]
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BALE/c;
RX MEDLINE=20148788; PubMed=10681567;
RA Suzuki N., Ishizaki J., Yokota Y., Higashino K., Ono T., Ikeda M.,
RA Fujii N., Kawamoto K., Hanasaki K.;
RT "Structures, enzymatic properties, and expression of novel human and
RT mouse secretory phospholipase A(2)s."
RL J. Biol. Chem. 275:5785-5793(2000).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H2O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in uterus, and at lower

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CC levels in various other tissues.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.
CC -----
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CC -----
CC EMBL; AF166098; AAF04499.1; -.
CC EMBL; AF112984; AAF22290.1; -.
CC HSP; P14555; IPOD.
CC MGD; MGI:1349660; Pla2g2a.
CC InterPro; IPR001211; PhospholipaseA2.
CC Pfam; PF00068; phoslip; 1.
CC PRINTS; PRO0389; PHPLIPASEA2.
CC ProDom; PD000303; PhospholipaseA2; 1.
CC SMART; SM00085; PA2c; 1.
CC PROSITE; PS00119; PA2_ASP; FALSE_NEG.
CC PROSITE; PS00118; PA2_HIS; 1.
CC Hydrolase; Lipid degradation; Signal; Calcium.
KW SIGNAL
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 142 GROUP IIE SECRETORY PHOSPHOLIPASE A2.
FT ACT SITE 65 65 BY SIMILARITY.
FT ACT SITE 109 109 BY SIMILARITY.
FT DISULFID 44 135 BY SIMILARITY.
FT DISULFID 46 62 BY SIMILARITY.
FT DISULFID 61 115 BY SIMILARITY.
FT DISULFID 67 142 BY SIMILARITY.
FT DISULFID 68 108 BY SIMILARITY.
FT DISULFID 77 101 BY SIMILARITY.
FT DISULFID 95 106 BY SIMILARITY.
FT METAL 45 45 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 49 49 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 66 66 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 142 AA; 15942 MW; 8B0E3CC710A1F946 CRC64;

Query Match 91.7%; Score 662; DB 1; Length 142;
Best Local Similarity 88.6%; Pred. No. 1.6e-64;
Matches 109; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 1 NLVFGVMIERTGKSAQYNDYCYCGIGGSHWVPDQTDWCHAHDCCYGRLEKLGCEP 60
DB 20 NLVFGVMIERTGKSAQYNDYCYCGIGGSHWVPDQTDWCHAHDCCYGRLEKLGCEP 79
QY 61 KLEKYLFSVSEGIIFCAGRTTCORLTCECDKRAALCFRNLTGNRYKVAHYPNKLTGTPT 120
DB 80 KLEKYLFSITRDNIFCAGRTACQRTCECDKRAALCFRNLTGNRYKVAHYPNKLTGTPT 139
QY 121 PPC 123
DB 140 PPC 142

RESULT 3
PA21 ERIMA
ID PA21 ERIMA STANDARD; PRT; 121 AA.
AC P24293;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 isozyme PLA-1 (EC 3.1.1.4) (Phosphatidylcholine
DE 2-acylhydrolase).
OS Eristocophis macmahoni (Leaf-nosed viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Viperinae; Eristocophis.

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OX NCBI\_TaxID=8702;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Venom;  
RX MEDLINE=92037623; PubMed=1935962;  
RA Siddiqui A.R., Zaidi Z.H., Joernvall H.;  
RT "Purification and characterization of two highly different group II  
RT phospholipase A2 isozymes from a single viperid (Eristocophis  
RT macmahoni) venom.";  
RL Eur. J. Biochem. 201:675-679 (1991).  
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
CC acyl groups in 3-sn-phosphoglycerides.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
CC acylglycerophosphocholine + a fatty acid anion.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II  
CC subfamily.  
DR PR; S17860; S17860.  
DR HSP; P81458; 1VIP.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR PRINTS; PR00389; PHPLIPASEA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR SMART; SM00085; PA2c; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
KW Hydrolase; Lipid degradation; Calcium; Multigene family.  
FT ACT\_SITE 47 47  
FT ACT\_SITE 89 89  
FT ACT\_SITE 26 115  
FT DISULFID 28 44  
FT DISULFID 43 95  
FT DISULFID 49 121  
FT DISULFID 50 88  
FT DISULFID 57 81  
FT DISULFID 75 86  
FT METAL 27 27  
FT METAL 29 29  
FT METAL 31 31  
FT METAL 48 48  
SQ SEQUENCE 121 AA; 13533 MW; F5BA64676954B5E CRC64;  
Query Match 51.5%; Score 372; DB 1; Length 121;  
Best Local Similarity 56.5%; Pred. No. 2.8e-33;  
Matches 70; Conservative 8; Mismatches 42; Indels 4; Gaps 3;  
Qy 1 NLVQFGWVIEKMTGKSA-LOYNDYGCYCGIGGSHWPVDQTDWCHADCCYGRLEKLGCE 59  
Db 1 NLVQFGKVI FMTGKSAALLSYDYGCGWGGKGLPDA'DRCFCVHDCCYGRVN--GCN 58  
Qy 60 PKLEKLYFSVSRGIFGAGRTTCQRLTCECDKAAALCFRNLGTYNRKYAHYPNKLCITGP 119  
Db 59 PKLSTYSYFQNGDIVCGDDNACLRAVCECDRAAICFGENLNTYDRKYKDYPSQCT-E 117  
Qy 120 TPPC 123  
Db 118 TEQC 121  
RESULT 4  
PA2A\_HUMAN STANDARD; PRT; 144 AA.  
AC P14555; Q9UCD2;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)  
DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)  
DE (GIIC sPLA2) (Non-pancreatic secretory phospholipase A2) (NPS-PLA2).

GN PLA2G2A OR PLA2B OR RASP-A OR PLA2L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX TISSUE=Rheumatoid arthritic synovial fluid;  
RX MEDLINE=89174566; PubMed=2925608;  
RA Seihamer J.J., Pruzanski W., Vadas P., Plant S., Miller J.A.,  
RA Kloss J., Johnson L.K.;  
RT "Cloning and recombinant expression of phospholipase A2 present in  
RT rheumatoid arthritic synovial fluid.";  
RL J. Biol. Chem. 264:5335-5338 (1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89174633; PubMed=2925633;  
RA Kramer R.M., Hession C., Johansen B., Hayes G., McGray P., Chow E.P.,  
RA Tizard R., Pepinsky R.B.;  
RT "Structure and properties of a human non-pancreatic phospholipase  
RT A2.";  
RL J. Biol. Chem. 264:5768-5775 (1989).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91050834; PubMed=2239446;  
RA Kramer R.M., Johansen B., Hession C., Pepinsky R.B.;  
RT "Structure and properties of a secreted phospholipase A2 from human  
RT platelets.";  
RL Adv. Exp. Med. Biol. 275:35-53 (1990).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
RT human and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [5]  
RP SEQUENCE OF 21-144.  
RC TISSUE=Spleen;  
RX MEDLINE=89374261; PubMed=2775276;  
RA Kanda A., Ono T., Yoshida N., Tojo H., Okamoto M.;  
RT "The primary structure of a membrane-associated phospholipase A2 from  
RT human spleen.";  
RL Biochem. Biophys. Res. Commun. 163:42-48 (1989).  
RN [6]  
RP SEQUENCE OF 21-54.  
RC TISSUE=Synovial fluid;  
RX MEDLINE=89197814; PubMed=3240982;  
RA Hara S., Kudo I., Matsuta K., Miyamoto T., Inoue K.;  
RT "Amino acid composition and NH2-terminal amino acid sequence of human  
RT phospholipase A2 purified from rheumatoid synovial fluid.";  
RL J. Biochem. 104:326-328 (1988).  
RN [7]  
RP SEQUENCE OF 21-33.  
RC TISSUE=Synovial fluid;  
RX MEDLINE=89076274; PubMed=3202859;

RA Lai C.Y., Wada K.;  
 RT "Phospholipase A2 from human synovial fluid: purification and  
 RT structural homology to the placental enzyme.";  
 RL Biochem. Biophys. Res. Commun. 157:488-493(1988).  
 RN (8)  
 RP SEQUENCE OF 21-75.  
 RC TISSUE=ileal mucosa;  
 RA MEDLINE=94002200; PubMed=8399335;  
 RX MEDLINE=91287826; PubMed=2062381;  
 RA Wery J.-P., Schevitz R.W., Clawson D.K., Bobbitt J.L., Dow E.R.,  
 RA Gamboa G., Goodson T. Jr., Hermann R.B., Kramer R.M., McClure D.B.,  
 RA Mihelich E.D., Putnam J.E., Sharp J.D., Stark D.H., Teater C.,  
 RA Warrick M.W., Jones N.D.;  
 RT "Structure of recombinant human rheumatoid arthritic synovial fluid  
 RT phospholipase A2 at 2.2-A resolution.";  
 RL Nature 352:79-82(1991).  
 RN (10)  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=92054586; PubMed=1948070;  
 RA Scott D.L., White S.P., Browning J.L., Rosa J.J., Gelb M.H.,  
 RA Sigler P.B.;  
 RT "Structures of free and inhibited human secretory phospholipase A2  
 RT from inflammatory exudate.";  
 RL Science 254:1007-1010(1991).  
 RN (11)  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=93393225; PubMed=7664108;  
 RA Schvitz R.W., Bach N.J., Carlson D.G., Chirgadze N.Y., Clawson D.K.,  
 RA Dillard R.D., Draheim S.E., Hartley L.W., Jones N.D., Mihelich E.D.,  
 RA Olkowski J.L., Snyder D.W., Dand S.C., Wery J.-P.;  
 RT "Structure-based design of the first potent and selective inhibitor  
 RT of human non-pancreatic secretory phospholipase A2";  
 RL Nat. Struct. Biol. 2:458-465(1995).  
 RN (12)  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RX MEDLINE=98207049; PubMed=9538252;  
 RA Kitadokoro K., Hagishita S., Sato T., Ohtan M., Miki K.;  
 RT "Crystal structure of human secretory phospholipase A2-IIA complex  
 RT with the potent indolizine inhibitor 120-1032.";  
 RL J. Biochem. 123:619-623(1998).  
 CC -!- FUNCTION: Thought to participate in the regulation of the  
 CC phospholipid metabolism in biomembranes including eicosanoid  
 CC biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-  
 CC acyl groups in 3-sn-phosphoglycerides.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 CC acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.  
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.  
 CC -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells  
 CC and also extracellularly. The membrane-bound and secreted forms  
 CC are identical and are encoded by a single gene.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M22430; AAA36550.1; -;  
 CC EMBL; M22431; AAA36549.1; -;  
 CC EMBL; BC005919; AAH05919.1; -;  
 CC FIR; A32862; PSUYF;  
 CC PDB; 1AYP; 31-JUL-95.  
 CC PDB; 1BBC; 31-OCT-93.

DR PDB; 1POD; 31-OCT-93.  
 DR PDB; 1POE; 31-OCT-93.  
 DR PDB; 1KVO; 07-JUL-97.  
 DR PDB; 1DB4; 12-NOV-99.  
 DR PDB; 1DB5; 12-NOV-99.  
 DR PDB; 1DCY; 12-NOV-99.  
 DR Genew; HGNC:9031; FLA2G2A.  
 DR MIM; 172411; -;  
 DR GO; GO:0004623; F:phospholipase A2 activity; TAS.  
 DR InterPro; IPR001211; PhospholipaseA2.  
 DR Pfam; PF00068; phoslip; 1.  
 DR PRINTS; PR00389; PHPLIPASEA2.  
 DR ProDom; PD000303; PhospholipaseA2; 1.  
 DR SMART; SM00085; PAZC; 1.  
 DR PROSITE; PS00118; PA2\_HIS; 1.  
 DR PROSITE; PS00119; PA2\_ASP; 1.  
 KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium;  
 KW 3D-structure.  
 FT SIGNAL 1 20  
 FT CHAIN 21 144  
 FT ACT\_SITE 67 67  
 FT ACT\_SITE 111 111  
 FT DISULFID 46 137  
 FT DISULFID 48 64  
 FT DISULFID 63 117  
 FT DISULFID 69 144  
 FT DISULFID 70 110  
 FT DISULFID 79 103  
 FT DISULFID 97 108  
 FT METAL 47 47  
 FT METAL 49 49  
 FT METAL 51 51  
 FT METAL 68 68  
 FT METAL 22 33  
 FT HELIX 37 40  
 FT TURN 41 41  
 FT TURN 45 47  
 FT HELIX 59 75  
 FT TURN 76 78  
 FT TURN 88 91  
 FT TURN 92 93  
 FT STRAND 94 94  
 FT HELIX 102 120  
 FT TURN 121 121  
 FT HELIX 122 124  
 FT TURN 127 128  
 Query Match 49.9%; Score 360.5; DB 1; Length 144;  
 Best Local Similarity 55.6%; Pred. No. 5.9e-32;  
 Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;  
 QY 1 NLVQFQVMIERTGK-SALQVNDYCYGICIGSHWPFVDQTCCHADCCYGRLEKLGCE 59  
 Db 21 NLVNFHRMFKLTGTKEAALSFGYCHGCVGSGSPKDATDRCCVTHDCCYKLEKRGCG 80  
 QY 60 PKLEYLPSVSRGIFCAGRTTCQELTCECDKRALCFERNLGTNRKYAHVPNKLCTGP 119  
 Db 81 TKFLSYKFSNGSRITCARQDSRQSCQLCECDRAAATCFARNKTTINKYQYYSNKHCRGS 140  
 QY 120 TPPC 123  
 Db 141 TPRC 144  
 RESULT 5  
 PA2 CERCE STANDARD; PRT; 120 AA.  
 AC P21789;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-MAY-1991 (Rel. 18, Last sequence update)  
 DE 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).  
 OS Cerastes cerastes (Horned desert viper).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Cerastes.  
 OX NCBI\_TaxID=8697;  
 RN [1]  
 RN SEQUENCE.  
 RP STRAIN=Baluchistan; TISSUE=Venom;  
 RC MEDLINE=91130587; PubMed=1993470;  
 RX Siddiqi A.R., Shafat J., Zaidi Z.H., Joernvall H.;  
 RA "Characterization of phospholipase A2 from the venom of Horned viper  
 RT (Cerastes cerastes).";  
 RL FEBS Lett. 278:14-16 (1991).  
 RN [2]  
 RN SEQUENCE OF 1-31.  
 RP STRAIN=Tunisia; TISSUE=Venom;  
 RC MEDLINE=90385487; PubMed=2402760;  
 RX Djebbari F.L., Martin-Baucalire M.-F.;  
 RA "Purification and characterization of a phospholipase A2 from  
 RT Cerastes cerastes (horn viper) snake venom.";  
 RL Toxicon 28:637-646 (1990).  
 RN [1]  
 RN FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
 CC acyl groups in 3-sn-phosphoglycerides.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 CC acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- MISCELLANEOUS: Strains variations are extensive for this enzyme.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II  
 CC subfamily.  
 DR PIR; A35950; A35950.  
 DR PIR; S13019; S13019.  
 DR HSSP; P81458; 1VIP.  
 DR InterPro; IPR001211; PhospholipaseA2.  
 DR Pfam; PF00068; Phoslip; 1.  
 DR PRINTS; PR00389; PHPLIPASEA2.  
 DR PRODOM; PD000303; PhospholipaseA2; 1.  
 DR SMART; SM00085; PA2C; 1.  
 DR PROSITE; PS00119; PA2\_ASP; 1.  
 DR PROSITE; PS00118; PA2\_HIS; 1.  
 DR Hydrolase; Lipid degradation; Calcium.  
 FT ACT\_SITE 47 47  
 FT ACT\_SITE 47 47  
 FT ACT\_SITE 89 89  
 FT DISULFID 26 115  
 FT DISULFID 28 44  
 FT DISULFID 43 95  
 FT DISULFID 50 88  
 FT DISULFID 57 81  
 FT DISULFID 75 86  
 FT METAL 27 27  
 FT METAL 29 29  
 FT METAL 31 31  
 FT METAL 48 48  
 FT VARIANT 10 12  
 FT VARIANT 17 19  
 FT VARIANT -22 23  
 SQ SEQUENCE 120 AA; 13534 MW; E6581FA7001C62C3 CRC64;  
 Query March 49.7%; Score 358.5; DB 1; Length 120;  
 Best Local Similarity 54.2%; Pred. No. 8e-32;  
 Matches 64; Conservative 10; Mismatches 41; Indels 3; Gaps 2;  
 QY 1 NLVQGVNIEKGTGKSAI-QYNDYGCYGGIGGSHWPVDQDWCHADCCYGRLEKLGCE 59  
 D5 1 NLVQGVNIEKGTGKSAI-QYNDYGCYGGIGGSHWPVDQDWCHADCCYGRLEKLGCE 59  
 QY 60 PLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLTGTNRYKHYHYNKLC 117  
 D5 59 PKRTSYSPQNGGIIVCDQNLCKRAVCECDRAAICFGENVNTYDKKYDYPTSOCT 116

RESULT 6  
 ID PA2N VIPAA STANDARD; PRT; 137 AA.  
 AC P34180; Q91967;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Phospholipase A2, neutral precursor (EC 3.1.1.4) (Ammodontin I2)  
 DE (Phosphatidylcholine 2-acylhydrolase).  
 GN AMI2.  
 OS Vipera ammodytes ammodytes (Western sand viper).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Vipera.  
 OX NCBI\_TaxID=8705;  
 RN [1]  
 RN SEQUENCE FROM N.A., AND SEQUENCE OF 17-137.  
 RP TISSUE=Venom gland;  
 RX MEDLINE=92201190; PubMed=1551386;  
 RA Krizaj I., Liang N.-S., Pungercar J., Strukelj B., Ritonja A.,  
 RA Gubensek F.;  
 RT "Amino acid and cDNA sequences of a neutral phospholipase A2 from the  
 RL long-nosed viper (Vipera ammodytes ammodytes) venom.";  
 RL Eur. J. Biochem. 204:1057-1062 (1992).  
 RN [2]  
 RP REVISION TO 132.  
 RA Pungercar J.;  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RA Kordis D., Gubensek F.;  
 RT "Molecular evolution of phospholipase A2 multigene family in Vipera  
 ammodytes";  
 RL Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
 CC acyl groups in 3-sn-phosphoglycerides.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 CC acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II  
 CC subfamily.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X56878; CAA40200.2; -.  
 CC EMBL; X84018; CAA58840.1; -.  
 CC PIR; S22388; S22388.  
 CC HSSP; P81458; 1VIP.  
 CC InterPro; IPR001211; PhospholipaseA2.  
 CC Pfam; PF00068; Phoslip; 1.  
 CC PRINTS; PR00389; PHPLIPASEA2.  
 CC PRODOM; PD000303; PhospholipaseA2; 1.  
 CC SMART; SM00085; PA2C; 1.  
 CC PROSITE; PS00119; PA2\_ASP; 1.  
 CC PROSITE; PS00118; PA2\_HIS; 1.  
 CC Hydrolase; Lipid degradation; Calcium; Signal;  
 KW Multigene family.  
 FT SIGNAL 1 16  
 FT CHAIN 17 137 PHOSPHOLIPASE A2, NEUTRAL.  
 FT ACT\_SITE 63 63 BY SIMILARITY.  
 FT ACT\_SITE 105 105 BY SIMILARITY.  
 FT DISULFID 42 131 BY SIMILARITY.  
 FT DISULFID 44 60 BY SIMILARITY.  
 FT DISULFID 59 111 BY SIMILARITY.  
 FT DISULFID 65 137 BY SIMILARITY.  
 FT DISULFID 66 104 BY SIMILARITY.

FT DISULFID 73 97 BY SIMILARITY.  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT METAL 43 43 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL 45 45 (BY SIMILARITY).  
 FT METAL 47 47 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL 47 47 (BY SIMILARITY).  
 FT METAL 64 64 CALCIUM (VIA CARBONYL OXYGEN)  
 FT METAL 64 64 (BY SIMILARITY).  
 SQ SEQUENCE 137 AA; 15309 MW; BDEC100B7F524431 CRC64;  
 Query Match 49.6%; Score 358; DB 1; Length 137;  
 Best Local Similarity 54.8%; Pred. No. 1e-31;  
 Matches 68; Conservative 11; Mismatches 41; Indels 4; Gaps 3;  
 QY 1 NLVQGVMIKWTGKSA-LQNDYGCYCGIGGSHWPDQDWCCHAHDCVGRLEKLGCE 59  
 DB 17 NLYQFGNMFQWTKSALLSYNSYNGCYGCGKGPQDADRCCFVHDCYGRV--GCD 74  
 QY 60 PKLEYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRNLGTNRKRYAHYPNKLTGTP 119  
 DB 75 PKLSYSPFNGDIVCGDDPCLRVCECDRAAICFGENLNTYDKKYNPSSHCT-E 133  
 QY 120 TPPC 123  
 DB 134 TEQC 137  
 RESULT 7  
 PA2\_DABRR STANDARD; PRT; 121 AA.  
 ID PA2\_DABRR STANDARD; PRT; 121 AA.  
 AC P81458;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Phospholipase A2 RVV-VD (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).  
 OS Daboia russelli russelli (Russell's viper) (Vipera russelli russelli).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Viperinae; Daboia.  
 OC NCBI\_TaxID=31159;  
 RN [1]  
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
 RC TISSUE=Venom;  
 RX MEDLINE=98267643; PubMed=9604284;  
 RA Carredano E., Westerlund B., Persson B., Saarinen M., Ramaswamy S., Eaker D., Eklund H.;  
 RT "The three-dimensional structures of two toxins from snake venom throw light on the anticoagulant and neurotoxic sites of phospholipase A2.";  
 RL Toxicol 36:75-92(1998).  
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides. This protein has anticoagulant activity.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1 calcium ion per subunit.  
 CC -!- SUBUNIT: Monomer.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.  
 DR PDB; 1VIP; 16-JUN-97.  
 DR InterPro; IPR001211; PhospholipaseA2.  
 DR Pfam; PF00068; phoslip.1.  
 DR PRINTS; PR00389; PHPLIPASEA2.  
 DR ProDom; PD000303; PhospholipaseA2; 1.  
 DR SMART; SM00085; PA2c; 1.  
 DR PROSITE; PS00119; PA2\_ASP; 1.  
 DR PROSITE; PS00118; PA2\_HIS; 1.  
 KW Hydrolase; Lipid degradation; Calcium; 3D-structure.  
 FT ACT\_SITE 47 47  
 FT ACT\_SITE 89 89

FT DISULFID 26 115  
 FT DISULFID 28 44  
 FT DISULFID 43 95  
 FT DISULFID 49 121  
 FT DISULFID 50 88  
 FT DISULFID 57 81  
 FT DISULFID 75 86  
 FT METAL 27 27  
 FT METAL 29 29  
 FT METAL 31 31  
 FT METAL 48 48  
 FT HELIX 2 13  
 FT HELIX 17 20  
 FT STRAND 23 24  
 FT TURN 25 27  
 FT STRAND 28 29  
 FT HELIX 39 53  
 FT TURN 54 54  
 FT HELIX 55 57  
 FT TURN 59 61  
 FT STRAND 66 68  
 FT STRAND 73 75  
 FT HELIX 80 98  
 FT TURN 99 102  
 FT HELIX 105 107  
 FT STRAND 108 108  
 FT TURN 109 109  
 FT HELIX 112 114  
 SQ SEQUENCE 121 AA; 13626 MW; 98CBC4A8922A89D1 CRC64;  
 Query Match 49.2%; Score 355; DB 1; Length 121;  
 Best Local Similarity 53.2%; Pred. No. 1.9e-31;  
 Matches 66; Conservative 13; Mismatches 41; Indels 4; Gaps 3;  
 QY 1 NLVQGVMIKWTGKSA-LQNDYGCYCGIGGSHWPDQDWCCHAHDCVGRLEKLGCE 59  
 DB 1 NLQFAEIVMTGNPLSSSDYGCYCGKGPQDADRCCFVHDCYGRV--SCK 58  
 QY 60 PKLEYLFSVSERGIFCAGRTTCORLTCECDKRAALCFRNLGTNRKRYAHYPNKLTGTP 119  
 DB 59 PKLSYSPFNGDIVCGDDPCLRVCECDRAAICFGENLNTYDKKYNPSSHCTG- 117  
 QY 120 TPPC 123  
 DB 118 TEQC 121  
 RESULT 8  
 PA21\_AGKPI STANDARD; PRT; 123 AA.  
 ID PA21\_AGKPI STANDARD; PRT; 123 AA.  
 AC P51372;  
 DT 01-OCT-1996 (Rel. 34; Created)  
 DT 15-JUL-1998 (Rel. 36; Last sequence update)  
 DT 10-OCT-2003 (Rel. 42; Last annotation update)  
 DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase) (APP-D-49).  
 OS Agkistrodon piscivorus piscivorus (Eastern cottonmouth).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Agkistrodon.  
 OC NCBI\_TaxID=8716;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Venom;  
 RX MEDLINE=93257049; PubMed=8489705;  
 RA Welches W., Reardon I.M., Heinrichson R.L.;  
 RT "An examination of structural interactions presumed to be of importance in the stabilization of phospholipase A2 dimers based upon comparative protein sequence analysis of a monomeric and dimeric enzyme from the venom of Agkistrodon p. piscivorus.";  
 RT

RL J. Protein Chem. 12:187-193(1993).  
RN [2]  
RP SEQUENCE OF 1-23, AND ACYLATION.  
RC TISSUE=Venom;  
RX MEDLINE=88298768; PubMed=3403524;  
RA Cho W., Tomasselli A.G., Heinrichson R.L., Kezdy F.J.;  
RT "The chemical basis for interfacial activation of monomeric  
RT phospholipase A2. Autocatalytic derivatization of the enzyme by acyl  
RT transfer from substrate.";  
RL J. Biol. Chem. 263:11237-11241(1988).  
RN [3]  
RP CHARACTERIZATION.  
RC TISSUE=Venom;  
RX MEDLINE=85054816; PubMed=6438084;  
RA Maraganore J.M., Merutka G., Cho W., Welches W., Kezdy F.J.,  
RA Heinrichson R.L.;  
RT "A new class of phospholipases A2 with lysine in place of aspartate  
RT 49. Functional consequences for calcium and substrate binding.";  
RL J. Biol. Chem. 259:13839-13843(1984).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).  
RC TISSUE=Venom;  
RX MEDLINE=97166209; PubMed=9013608;  
RA Han S.K., Yoon E.T., Scott D.L., Sigler P.B., Cho W.;  
RT "Structural aspects of interfacial adsorption. A crystallographic and  
RT site-directed mutagenesis study of the phospholipase A2 from the  
RT venom of Agkistrodon piscivorus piscivorus.";  
RL J. Biol. Chem. 272:3573-3582(1997).  
RN [5]  
RP FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
RP acyl groups in 3-sn-phosphoglycerides.  
RC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
RC acylglycerophosphocholine + a fatty acid anion.  
CC -1- COFACTOR: Binds 1 calcium ion per subunit.  
CC -1- SUBUNIT: Monomer or homodimer.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- PTM: Acylation causes dimerization.  
CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group II  
CC subfamily.  
DR PIR; B53872; B53872.  
DR FDB; LVAP; 07-JUL-97.  
DR InterPro; IPR001211; PhospholipaseA2.  
DR Pfam; PF00068; phoslip; 1.  
DR PRINTS; PF00389; PHPLIPASEA2.  
DR ProDom; PD000303; PhospholipaseA2; 1.  
DR SMART; SMC0085; PA2c; 1.  
DR PROSITE; PS00119; PA2\_ASP; 1.  
DR PROSITE; PS00118; PA2\_HIS; 1.  
KW Hydrolase; Lipid degradation; Calcium; Lipoprotein; Palmitate;  
KW 3D-structure.  
FT ACT\_SITE 47 47  
FT ACT\_SITE 89 89 BY SIMILARITY.  
FT DISULFID 26 116 BY SIMILARITY.  
FT DISULFID 28 44  
FT DISULFID 43 95  
FT DISULFID 49 123  
FT DISULFID 50 88  
FT DISULFID 57 81  
FT DISULFID 75 86  
FT METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN).  
FT METAL 29 29 CALCIUM (VIA CARBONYL OXYGEN).  
FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN).  
FT METAL 48 48 CALCIUM.  
FT LIPID 7 7 N(6)-palmitoyl lysine.  
FT LIPID 10 10 N(6)-palmitoyl lysine.  
FT HELIX 2 13  
FT HELIX 17 20  
FT STRAND 23 24  
FT TURN 25 27  
FT STRAND 28 29  
FT HELIX 39 52  
FT TURN 53 53  
FT TURN 59 61  
FT STRAND 66 69

FT TURN 70 71  
FT STRAND 72 75  
FT HELIX 80 98  
FT TURN 99 99  
FT HELIX 100 102  
FT HELIX 105 108  
FT STRAND 109 109  
FT TURN 110 110  
FT HELIX 113 116  
SQ SEQUENCE 123 AA; 13989 MW; C39986552D990D72 CRC64;  
  
Query Match 48.5%; Score 350; DB 1; Length 123;  
Best Local Similarity 52.0%; Pred. No. 6.8e-31;  
Matches 65; Conservative 14; Mismatches 42; Indels 4; Gaps 3;  
  
QY 1 NLVQGVMLEKMTGKSA-LQYNDYCYGICGSHWPVDOTWCCHAHDCCYCRLEKQCE 59  
Db 1 NLFQFEKLIKMTGKSGMLWYSAYCYCGWGQGGPKDARTCCFVHDCCKYK--TGCN 58  
QY 60 PKLEKYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRK-YAHYPNKLCTG 118  
Db 59 PRMDIYTVSDNGNIVCGTNPCKKQICECDRAAICFEDNLKTYDSKTYKPKKNCKE 118  
QY 119 PTPPC 123  
Db 119 ESEPC 123  
  
RESULT 9  
PA2A RAT STANDARD; PRT; 146 AA.  
ID PA2A RAT  
AC F14423;  
DT 01-JAN-1990 (Rel. 13, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)  
DE (Phosphatidylcholine 2-acylhydrolase) (group IIA phospholipase A2)  
DE (GIIC SPLA2).  
GN PLA2G2A.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Platelet;  
RX MEDLINE=90110043; PubMed=2606907;  
RA Komada M., Kudo I., Mizushima H., Kitamura N., Inoue K.;  
RT "Structure of cDNA coding for rat platelet phospholipase A2.";  
RL J. Biochem. 106:545-547(1989).  
RN [2]  
SEQUENCE FROM N.A.  
RC TISSUE=Spleen;  
RX MEDLINE=90267443; PubMed=2346480;  
RA Komada M., Kudo I., Inoue K.;  
RT "Structure of gene coding for rat group II phospholipase A2.";  
RL Biochem. Biophys. Res. Commun. 168:1059-1065(1990).  
RN [3]  
SEQUENCE FROM N.A.  
RX MEDLINE=89350908; PubMed=2764915;  
RA Ishizaki J., Ohara O., Nakamura E., Tamaki M., Ono T., Kanda A.,  
RA Yoshida N., Teraoka H., Tojo H., Okamoto M.;  
RT "cDNA cloning and sequence determination of rat membrane-associated  
RT phospholipase A2.";  
RL Biochem. Biophys. Res. Commun. 162:1030-1036(1989).  
RN [4]  
SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=90381322; PubMed=2400792;  
RA Kusunoki C., Satoh S., Kobayashi M., Niwa M.;  
RT "Structure of genomic DNA for rat platelet phospholipase A2.";  
RL Biochim. Biophys. Acta 1087:95-97(1990).  
RN [5]

SEQUENCE OF 22-146.  
 RC STRAIN=Wistar; TISSUE=Platelet;  
 RX MEDLINE=89174508; PubMed=3235451;  
 RA Hayakawa M., Kudo I., Tomita M., Nojima S., Inoue K.;  
 RT "The primary structure of rat platelet phospholipase A2.";  
 RL J. Biochem. 104:767-772(1988).  
 [6]  
 RN SEQUENCE OF 22-57.  
 RP TISSUE=Spleen;  
 RC MEDLINE=86186890; PubMed=3356705;  
 RA Ono T., Tojo H., Kuramitsu S., Kagamiyama H., Okamoto M.;  
 RT "Purification and characterization of a membrane-associated  
 phospholipase A2 from rat spleen. Its comparison with a cytosolic  
 phospholipase A2 S-1.";  
 RL J. Biol. Chem. 263:5732-5738(1988).  
 [7]  
 RN SEQUENCE OF 22-46.  
 RP TISSUE=Platelet;  
 RC MEDLINE=88007474; PubMed=3654593;  
 RA Hayakawa M., Horigome K., Kudo I., Tomita M., Nojima S., Inoue K.;  
 RT "Amino acid composition and NH2-terminal amino acid sequence of rat  
 platelet secretory phospholipase A2.";  
 RL J. Biochem. 101:1311-1314(1987).  
 [8]  
 RN SEQUENCE OF 22-45.  
 RP TISSUE=Liver;  
 RC MEDLINE=89253484; PubMed=2722857;  
 RA Aarsman A.J., de Jong J.G.N., Arnoldussen E., Neys F.W.,  
 van Wassenaer P.D., van den Bosch H.;  
 RT "Immunofluorescence purification, partial sequence, and subcellular  
 localization of rat liver phospholipase A2.";  
 RL J. Biol. Chem. 264:10008-10014(1989).  
 CC -!- FUNCTION: Thought to participate in the regulation of the  
 phospholipid metabolism in biomembranes including eicosanoid  
 biosynthesis. Catalyzes the calcium-dependent hydrolysis of the 2-  
 acyl groups in 3-sn-phosphoglycerides.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Membrane-associated.  
 CC -!- MISCELLANEOUS: Group II phospholipase A2 is found in many cells  
 and also extracellularly. The membrane-bound and secreted forms  
 are identical and are encoded by a single gene.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
 CC  
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 CC  
 CC EMBL; D00523; BAA0410.1; -  
 DR EMBL; M37127; AAA41223.1; -  
 DR EMBL; M25148; AAA41920.1; -  
 DR EMBL; X51529; CRA35909.1; -  
 DR PIR; A33394; A33394.  
 DR HSP; P14555; 1P0D.  
 DR InterPro; IPR001211; PhospholipaseA2.  
 DR Pfam; PF00068; phoslip\_1  
 DR PRINTS; PK00389; PHPLIPASEA2.  
 DR ProDom; PD000303; PhospholipaseA2; 1.  
 DR SMART; SM00085; PA2G; 1.  
 DR PROSITE; PS00118; PA2\_HIS; 1.  
 DR PROSITE; PS00119; PA2\_ASP; 1.  
 KW Hydrolase; Lipid degradation; Membrane; Signal; Calcium.  
 FT SIGNAL 1 21 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.  
 FT CHAIN 22 146  
 FT ACT\_SITE 68 68  
 FT ACT\_SITE 113 113  
 FT BY SIMILARITY.  
 FT DISULFID 47 139  
 FT BY SIMILARITY.  
 FT DISULFID 49 65

FT DISULFID 64 119 BY SIMILARITY.  
 FT DISULFID 70 146 BY SIMILARITY.  
 FT DISULFID 71 112 BY SIMILARITY.  
 FT DISULFID 80 105 BY SIMILARITY.  
 FT DISULFID 98 110 BY SIMILARITY.  
 FT METAL 48 48 CALCIUM (VIA CARBONYL OXYGEN)  
 (BY SIMILARITY).  
 FT METAL 50 50 CALCIUM (VIA CARBONYL OXYGEN)  
 (BY SIMILARITY).  
 FT METAL 52 52 CALCIUM (VIA CARBONYL OXYGEN)  
 (BY SIMILARITY).  
 FT METAL 69 69 CALCIUM (BY SIMILARITY).  
 FT VARIANT 135 135 P -> L (POLYMORPHISM).  
 FT CONFLICT 22 22 S -> D (IN REF. 8).  
 FT CONFLICT 63 63 W -> E (IN REF. 5).  
 FT CONFLICT 69 69 D -> E (IN REF. 5).  
 FT CONFLICT 78 78 R -> S (IN REF. 5).  
 FT CONFLICT 85 85 L -> V (IN REF. 3).  
 FT CONFLICT 121 121 L -> S (IN REF. 5).  
 FT SEQUENCE 145 AA; 16294 MW; 60DDC9E79BF109F7 CRC64;  
 SQ  
 Query Match 48.1%; Score 347; DB 1; Length 146;  
 Best Local Similarity 51.2%; Pred. No. 1.7e-30;  
 Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;  
 QY 1 NLVQFGVMIEKMTGKSA-LQYNDYCYGICGGSHWPDQTDWCCHADCCYGRLEKLGCE 59  
 DB 22 SLLEFGQMLPFTGKRVDSYGFYGCYGVGRSPKDATDCCVTHDCCYNRLKRGCG 81  
 QY 60 PKLEKLYFSVSERGIFCA-GRITQRLTCEDCKRAALCFRNLTGTYNRYAHYNNKLCGTG 118  
 DB 82 TKFLYKFSYRGGQISCTNQDSCKQLCQCDKAAACFAFNKKSYSLSKYQFYFNKFCGK 141  
 QY 119 PTPPC 123  
 DB 142 KTFPC 146  
 RESULT 10  
 PA2Q TRIFL STANDARD; PRT; 138 AA.  
 ID PA2Q TRIFL  
 AC Q8JIG0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Phospholipase A2 isozyme cPLA-B' (A) precursor (EC 3.1.1.4)  
 DE (Phosphatidylcholine 2-acylhydrolase).  
 OS Trimeresurus flavoviridis (Habu).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Lepidodonta; Squamata; Scieroglossa; Serpentes; Colubroidea;  
 OC Viperidae; Crotalinae; Trimeresurus.  
 OC NCBI\_TaxID=88087;  
 OX [1]  
 RN SEQUENCE FROM N.A.  
 RP STRAIN=Amami-Oshima, and Kagosima; TISSUE=Venom gland;  
 RC MEDLINE=22499762; PubMed=13612832;  
 RA Chijiwa T., Yamaguchi Y., Ogawa I., Deshimaru M., Nobuhisa I.,  
 RA Nakashima K.-I., Oda-Ueda N., Fukumaki Y., Hattori S., Onno M.;  
 RT "Interisland evolution of Trimeresurus flavoviridis venom  
 phospholipase A(2) isozymes.";  
 RL J. Mol. Evol. 56:286-293(2003).  
 CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the  
 2-acyl groups in 3-sn-phosphoglycerides.  
 CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 acylglycerophosphocholine + a fatty acid anion.  
 CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.  
 CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II  
 subfamily.  
 CC  
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EMBL; AB087496; BAC02719.1; --  
InterPro; IPR001211; PhospholipaseA2.  
Pfam; PF00068; Phoslip; 1.  
PRINTS; PR00389; PHPLIPASEA2.  
ProDom; PD000303; PhospholipaseA2; 1.  
SMART; SM00085; PA2c; 1.  
PROSITE; PS00119; PA2\_ASP; 1.  
PROSITE; PS00118; PA2\_HIS; 1.  
Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.  
FT SIGNAL 1 16  
FT CHAIN 17 138  
FT ACT\_SITE 63 63  
FT ACT\_SITE 105 105  
FT DISULFID 42 131  
FT DISULFID 44 60  
FT DISULFID 59 111  
FT DISULFID 65 104  
FT DISULFID 66 138  
FT DISULFID 73 97  
FT DISULFID 91 102  
FT METAL 43 43  
FT METAL 45 45  
FT METAL 47 47  
FT METAL 64 64  
SEQUENCE 138 AA; 15703 MW; CBDE540581DD2F10 CRC64;

Query Match 47.7%; Score 344.5; DB 1; Length 138;  
Best Local Similarity 50.0%; Pred. No. 3e-30;  
Matches 62; Conservative 15; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQFGVMIKMTGKSAAL-QYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59  
DB 17 HLLQFRKMKIKMTGKEPIVSVAFYGCYCGKGRGPKDATDRCCFVHDCCYGKV--TGCD 74  
QY 60 PKLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYKHYPNKLTCTGP 119  
DB 75 PKWDYTYVSSNGDIVCGDNPCTKEVCECDKAAAIACFRDNLKTYKRYWTFDFICTDP 134  
QY 120 TPPC 123  
DB 135 TEKC 138

RESULT 11  
PAZY\_TRIFL STANDARD; PRT; 138 AA.  
AC Q90Y77;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Phospholipase A2 isozyme PL-Y precursor (EC 3.1.1.4)  
DE (Phosphatidylcholine 2-acylhydrolase).  
OS Trimeresurus flavoviridis (Habu).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;  
OC Viperidae; Crotalinae; Trimeresurus.  
OX NCBI\_TaxID=89087;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Chijiwa T., Yamaguchi Y., Ogawa T., Deshimaru M., Nobuhisa I.,  
RA Nakashima K.-I., Oda-Ueda N., Shimohigashi Y., Fukumaki Y.,  
RA Hattori S., Ohno M.;  
RT "Regional evolution of Trimeresurus flavoviridis venom-gland phospholipase A2 isozymes.";

Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
-!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides (By similarity).  
-!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.  
-!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
-!- SUBCELLULAR LOCATION: Secreted (By similarity).  
-!- TISSUE SPECIFICITY: Expressed by the venom gland (Probable).  
-!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.

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EMBL; AB072173; BAB69546.1; --  
InterPro; IPR001211; PhospholipaseA2.  
Pfam; PF00068; Phoslip; 1.  
PRINTS; PR00389; PHPLIPASEA2.  
ProDom; PD000303; PhospholipaseA2; 1.  
SMART; SM00085; PA2c; 1.  
PROSITE; PS00119; PA2\_ASP; 1.  
PROSITE; PS00118; PA2\_HIS; 1.  
Hydrolase; Lipid degradation; Calcium; Multigene family; Signal.  
FT SIGNAL 1 16  
FT CHAIN 17 138  
FT ACT\_SITE 63 63  
FT ACT\_SITE 105 105  
FT DISULFID 42 131  
FT DISULFID 44 60  
FT DISULFID 59 111  
FT DISULFID 65 138  
FT DISULFID 66 104  
FT DISULFID 73 97  
FT DISULFID 91 102  
FT METAL 43 43  
FT METAL 45 45  
FT METAL 47 47  
FT METAL 64 64  
SEQUENCE 138 AA; 15729 MW; C96B1B878CCA1196 CRC64;

Query Match 47.7%; Score 344.5; DB 1; Length 138;  
Best Local Similarity 49.2%; Pred. No. 3e-30;  
Matches 61; Conservative 17; Mismatches 43; Indels 3; Gaps 2;

QY 1 NLVQFGVMIKMTGKSAAL-QYNDYGCYCGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59  
DB 17 HLLQFRKMKIKMTGKEPIVSVAFYGCYCGKGRGPKDATDRCCFVHDCCYGKV--TGCD 74  
QY 60 PKLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRYKHYPNKLTCTGP 119  
DB 75 PKWDYTYVSSNGDIVCGDNPCTKEVCECDKAAAIACFRDNLKTYKRYWTFDFICTDP 134  
QY 120 TPPC 123  
DB 135 TEKC 138

RESULT 12  
PAZA\_MOUSE STANDARD; PRT; 146 AA.  
ID PAZA\_MOUSE  
AC F31482; Q60871;  
DT 01-JUL-1993 (Rel. 26, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Phospholipase A2, membrane associated precursor (EC 3.1.1.4)

DE (Phosphatidylcholine 2-acylhydrolase) (Group IIA phospholipase A2)  
DE (Gric sPLA2) (Enhancing factor) (EF).  
GN PLA2G2A.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BALE/c;  
RA Mulherkar R.;  
RN Submitted (OCT-1994) to the EMBL/GenBank/DBSJ databases.  
[2]  
RP SEQUENCE FROM N.A., AND POLYMORPHISM.  
RC STRAIN=BALE/c, and CD-1, TISSUE=intestine;  
RX MEDLINE=9403435; PubMed=7673223;  
RA Kennedy B.P., Payette P., Mudgett J., Vadas P., Pruzanski W.,  
RA Yvan M., Tang C., Rancourt D.E., Cromlish W.;  
RT "A natural disruption of the secretory group II phospholipase A2 gene  
in inbred mouse strains.";  
RL J. Biol. Chem. 270:22378-22385(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C3H;  
RX MEDLINE=95300227; PubMed=7781071;  
RA MacPhee M., Chepenik K.P., Liddell R.A., Nelson K.K., Siracusa L.D.,  
RA Buchberg A.M.;  
RT "The secretory phospholipase A2 gene is a candidate for the Mom1  
locus, a major modifier of ApcMin-induced intestinal neoplasia.";  
RL Cell 81:957-966(1995).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Richards S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [5]  
RP SEQUENCE OF 22-146 FROM N.A.  
RC STRAIN=BALE/c; TISSUE=Small intestine;  
RX MEDLINE=94029555; PubMed=8267767;  
RA Mulherkar R., Rao R.S., Wagie A.S., Patki V., Deo M.G.;  
RT "Enhancing factor, a Paneth cell specific protein from mouse small  
intestines: predicted amino acid sequence from RT-PCR amplified cDNA  
and its expression.";  
RL Biochem. Biophys. Res. Commun. 195:1254-1263(1993).  
RN [6]  
RP ERRATUM.  
RX MEDLINE=94071967; PubMed=8250944;  
RA Mulherkar R., Rao R.S., Wagie A.S., Patki V., Deo M.G.;  
RL Biochem. Biophys. Res. Commun. 197:351-352(1993).  
RN [7]  
RP PRELIMINARY SEQUENCE OF 22-41.  
RC TISSUE=Small intestine;  
RX MEDLINE=93146172; PubMed=8425615;  
RA Mulherkar R., Rao R., Rao L., Patki V., Chauhan V.S., Deo M.G.;

RT "Enhancing factor protein from mouse small intestines belongs to the  
RT phospholipase A2 family.";  
RL FEBS Lett. 317:263-266(1993).  
CC -!- FUNCTION: May play a role in cell proliferation, by increasing the  
CC binding of EGF to the cells and thereby modulating its action. In  
CC doing so, this isozyme binds to a membrane-associated receptor  
CC distinct from the EGF receptor and which could be a heparan-  
CC sulfate proteoglycan located on the cell membrane.  
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
CC acyl groups in 3-sn-phosphoglycerides.  
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
CC acylglycerophosphocholine + a fatty acid anion.  
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).  
CC -!- SUBCELLULAR LOCATION: Membrane-associated.  
CC -!- TISSUE SPECIFICITY: Mainly in the Paneth cells adjacent to the  
CC stem population in the small intestines. Also expressed in  
CC regenerating liver and hyperplastic esophageal epithelium.  
CC -!- POLYMORPHISM: In strains 129/Sv, B10.RII and C57BL/6, a  
CC polymorphism causes a frameshift and premature truncation of the  
CC protein, rendering it inactive. Strains BALB/c, C3H/He, DBA/1,  
CC DBA/2, MRL and NZB/BlN contain the normal protein while strain CD-  
CC 1 is heterozygous for the mutation.  
CC -!- SIMILARITY: Belongs to the phospholipase A2 family.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: X74266; CAA52325.1; -  
CC EMBL: U32358; AAC52252.1; -  
CC EMBL: U28244; AAB06315.1; ALT INIT.  
CC EMBL: BC045156; AAH45156.1; -  
CC PIR: I48342; I48342.  
CC PIR: S29495; S29495.  
CC HSP: P14555; IPOB.  
CC MGD: MG1:104642; Pla2g2a.  
CC InterPro: IPR001211; PhospholipaseA2.  
CC Pfam: PF00068; phoslip; 1.  
CC PRINTS: PR00389; PHPLIPAS2A2.  
CC ProDom: PD000303; PhospholipaseA2; 1.  
CC SMART: SM00085; PA2C; 1.  
CC PROSITE: PS00118; PA2\_HIS; 1.  
CC PROSITE: PS00119; PA2\_ASP; 1.  
CC Hydrolase; Lipid degradation; Calcium; Growth regulation; Signal;  
CC Membrane; Polymorphism.  
CC SIGNAL 1 21  
CC CHAIN 22 146 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED.  
CC ACT\_SITE 68 68 BY SIMILARITY.  
CC ACT\_SITE 113 113 BY SIMILARITY.  
CC DISULFID 47 139 BY SIMILARITY.  
CC DISULFID 49 65 BY SIMILARITY.  
CC DISULFID 64 119 BY SIMILARITY.  
CC DISULFID 70 146 BY SIMILARITY.  
CC DISULFID 71 112 BY SIMILARITY.  
CC DISULFID 80 105 BY SIMILARITY.  
CC DISULFID 98 110 BY SIMILARITY.  
CC METAL 48 48 CALCIUM (VIA CARBONYL OXYGEN)  
CC METAL 50 50 (BY SIMILARITY).  
CC METAL 52 52 CALCIUM (VIA CARBONYL OXYGEN)  
CC METAL 52 52 (BY SIMILARITY).  
CC METAL 69 69 CALCIUM (VIA CARBONYL OXYGEN)  
CC METAL 19 19 V -> D (IN REF. 1).  
CC CONFLICT 86 86 K -> T (IN REF. 1).  
CC CONFLICT 86 86  
CC SEQUENCE 146 AA; 16145 MW; AB304F6B3B1BA5C7 CRC64;  
CC  
CC Query Match 47.2%; Score 341; DB 1; Length 146;  
CC Best Local Similarity 52.8%; Pred. No. 7.6e-30;





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FT DISULFID 74 85 BY SIMILARITY.
FT METAL 26 26 CALCIUM (VIA CARBONYL OXYGEN)
FT FT (BY SIMILARITY).
FT METAL 28 28 CALCIUM (VIA CARBONYL OXYGEN)
FT FT (BY SIMILARITY).
FT METAL 30 30 CALCIUM (VIA CARBONYL OXYGEN)
FT FT (BY SIMILARITY).
FT METAL 47 47 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 121 AA; 13363 MW; DC0500A87839E504 CRC64;

Query Match 47.1%; Score 340; DB 1; Length 121;
Best Local Similarity 47.2%; Pred. No. 8e-30;
Matches 58; Conservative 15; Mismatches 48; Indels 2; Gaps 1;

QY 1 NLVQFVMIKMTGKSLQYNDYCYGIGSHWPVDQWCHAHDCCYGRLEKLGCEP 60
DB 1 NLIQFGNMISAMTGKSLAVASYCYGCGWGGKQPKDTRCCFVHDCCYGKADK--CSP 58
QY 61 KLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRYAHYPNKLCTGPT 120
DB 59 KMILSYKFNHNGVCGDKNACKKKVCECDRVAALCFPAASKHSYNKULWRYPPSSKCTGTA 118
QY 121 PPC 123
DB 119 EKC 121

RESULT 15
PA2X_TRIFL STANDARD; PRT; 122 AA.
ID PA2X_TRIFL
AC P06860;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Phospholipase A2 isozyme PL-X (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase).
OS Trimeresurus flavoviridis (Habu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=89087;
RN [1]
RP SEQUENCE.
RC TISSUE=venom;
RX MEDLINE=87179112; PubMed=3564060;
RA Kiri R.M., Kawabata S.-I., Iwanaga S.;
RT "Comparison of amino terminal region of three isoenzymes of phospholipases A2 (TPV PL-Ia, TPV PL-Ib, TPV PL-X) from Trimeresurus flavoviridis (habu snake) venom and the complete amino acid sequence of the basic phospholipase, TPV PL-X."
RL Toxicon 24:1117-1123(1986).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the phospholipase A2 family. Group II subfamily.
DR PIR; A25500; PSTVXF.
DR HSSP; P51972; IVAP.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR PRINTS; PR00389; PHPLIPASEA2.
DR ProDom; PDO00303; PhospholipaseA2; 1.
DR SMART; SM00085; PA2C; 1.
DR PROSITE; PS00119; PA2_ASP; FALSE_NEG.
DR PROSITE; PS00118; PA2_HIS; 1.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT ACT_SITE 47 47 BY SIMILARITY.
FT ACT_SITE 89 89 BY SIMILARITY.
FT DISULFID 26 115 BY SIMILARITY.

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FT DISULFID 28 44 BY SIMILARITY.
FT DISULFID 43 95 BY SIMILARITY.
FT DISULFID 49 122 BY SIMILARITY.
FT DISULFID 50 88 BY SIMILARITY.
FT DISULFID 57 81 BY SIMILARITY.
FT DISULFID 75 86 BY SIMILARITY.
FT METAL 27 27 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 29 29 CALCIUM (BY SIMILARITY).
FT METAL 31 31 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 48 48 CALCIUM (VIA CARBONYL OXYGEN)
FT METAL 48 48 CALCIUM (BY SIMILARITY).
SQ SEQUENCE 122 AA; 13981 MW; A9D652276C5D0DF0 CRC64;

Query Match 47.0%; Score 339.5; DB 1; Length 122;
Best Local Similarity 49.2%; Pred. No. 9.2e-30;
Matches 61; Conservative 16; Mismatches 44; Indels 3; Gaps 2;

QY 1 NLVQFVMIKMTGKSLQYNDYCYGIGSHWPVDQWCHAHDCCYGRLEKLGCE 59
DB 1 HLQPRKMIKMTGKEPIVSVAFYCYCGKGRGPKDATDRCCFVHDCCYEKV--TGCD 58
QY 60 PKLEYLFSVSRGIFCAGRTTCQRLTCECDKRAALCFERNLGTYNRYAHYPNKLCTGP 119
DB 59 PKMSYTYTSLNGDIVCGDPYCTKVKCECDKAAICFRDLNLTYNRYAHYPNKLCTGP 118
QY 120 TPPC 123
DB 119 TEGC 122

Search completed: July 3, 2004, 05:16:40
Job time : 9.81887 secs

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OM protein - protein search, using sw model

Run on: July 3, 2004, 05:15:00 ; Search time 12.5321 Seconds  
(without alignments)  
506.699 Million cell updates/sec

Title: US-10-088-092A-30\_COPY\_20\_142

Perfect score: 722

Sequence: 1 NLVQFGVMEIKMTGKSALQY.....YNRKVAHYENKLTGPTTPPC 123

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
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6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	360.5	49.9	124	1	US-08-170-360-4
2	360.5	49.9	124	2	US-08-888-497-39
3	360.5	49.9	124	4	US-09-362-230-39
4	360.5	49.9	124	4	US-09-740-569-2
5	360.5	49.9	124	5	PCT-US94-07926-39
6	360.5	49.9	144	1	US-08-186-895-10
7	360.5	49.9	144	2	US-08-888-497-37
8	360.5	49.9	144	4	US-09-362-230-37
9	360.5	49.9	144	5	PCT-US94-07926-37
10	348	48.2	125	4	US-08-888-497-42
11	348	48.2	125	4	US-09-362-230-42
12	348	48.2	125	5	PCT-US94-07926-42
13	348	48.2	146	2	US-08-888-497-35
14	348	48.2	146	4	US-09-362-230-35
15	348	48.2	146	5	PCT-US94-07926-35
16	341	47.2	146	3	US-08-966-317-3
17	341	47.2	146	4	US-09-489-770-3
18	337	46.7	146	3	US-08-966-317-4
19	337	46.7	146	4	US-09-489-770-4
20	321	44.5	125	1	US-08-170-360-5
21	299.5	41.5	118	2	US-08-888-497-40
22	299.5	41.5	118	4	US-09-097-094-5
23	299.5	41.5	118	4	US-09-362-230-40
24	299.5	41.5	118	5	PCT-US94-07926-40
25	299.5	41.5	122	1	US-07-734-534A-1
26	299.5	41.5	138	2	US-08-888-497-32
27	299.5	41.5	138	4	US-09-362-230-32

28	299.5	41.5	138	5	PCT-US94-07926-32
29	296.5	41.1	117	2	US-08-888-497-44
30	296.5	41.1	117	4	US-09-362-230-44
31	296.5	41.1	117	5	PCT-US94-07926-44
32	296.5	41.1	137	2	US-08-888-497-30
33	296.5	41.1	137	4	US-09-362-230-30
34	296.5	41.1	137	5	PCT-US94-07926-30
35	287.5	39.8	165	3	US-08-966-317-1
36	287.5	39.8	165	4	US-09-489-770-1
37	286	39.6	130	2	US-08-888-497-43
38	286	39.6	130	4	US-09-362-230-43
39	286	39.6	130	5	PCT-US94-07926-43
40	286	39.6	158	2	US-08-888-497-22
41	286	39.6	158	4	US-09-362-230-22
42	286	39.6	158	5	PCT-US94-07926-22
43	244	33.8	118	3	US-09-090-602-4
44	226.5	31.4	126	1	US-08-170-360-3
45	226.5	31.4	126	2	US-08-888-497-38

ALIGNMENTS

RESULT 1  
US-08-170-360-4  
; Sequence 4, Application US/08170360  
; Patent No. 5656602  
; GENERAL INFORMATION:  
; APPLICANT: Teeng, Albert P. S.  
; APPLICANT: Ingllis, Adam  
; TITLE OF INVENTION: PLA2 INHIBITORY COMPOUNDS  
; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Rothwell, Perry Ernst & Kurz  
; STREET: Suite 701-E, 555 Thirteenth St., N.W  
; CITY: Washington  
; STATE: D. C.  
; COUNTRY: U.S.A.  
; ZIP: 20004

1997 (issued)

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA: US/08/170.360  
FILING DATE: 03-MAR-1994  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PCT/AU92/00333  
FILING DATE: 06-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: AU PK 7058  
FILING DATE: 04-JUL-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1871-104A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 124 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: N-terminal  
US-08-170-360-4

Query Match 49.9%; Score 360.5; DB 1; Length 124;  
Best Local Similarity 55.6%; Pred. No. 1.3e-31;  
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;  
QY 1 NLVQGVMIKMTGK-SALQYNDYGCYGGSHWPVDQTDWCHADCCYGRLEKLGCE 59  
DB 1 NLVNFHRMIKLTGTGKEALSFGFYCHGCVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60  
QY 60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119  
DB 61 TKFLSYKFSNGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKYQYYSNKHCRGS 120  
QY 120 TTPC 123  
DB 121 TPRC 124

## RESULT 2

US-08-888-497-39  
; Sequence 39, Application US/08888497  
; Patent No. 5972677  
; GENERAL INFORMATION:  
; APPLICANT: Tischfield, Jay A.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
; ADDRESSEE: Russell PA  
; STREET: 200 East Broward Boulevard  
; CITY: Fort Lauderdale  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 33301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/888,497  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/651,405  
; FILING DATE:  
; APPLICATION NUMBER: US 08/097,354  
; FILING DATE: 26-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Manso, Peter J.  
; REGISTRATION NUMBER: 32,264  
; REFERENCE/DOCKET NUMBER: IN21044-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 305-527-2498  
; TELEFAX: 305-764-4996  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-888-497-39

Query Match 49.9%; Score 360.5; DB 2; Length 124;  
Best Local Similarity 55.6%; Pred. No. 1.3e-31;  
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;  
QY 1 NLVQGVMIKMTGK-SALQYNDYGCYGGSHWPVDQTDWCHADCCYGRLEKLGCE 59

DB 1 NLVNFHRMIKLTGTGKEALSFGFYCHGCVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60  
QY 60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119  
DB 61 TKFLSYKFSNGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKYQYYSNKHCRGS 120  
QY 120 TTPC 123  
DB 121 TPRC 124  
RESULT 3  
US-09-362-230-39  
; Sequence 39, Application US/09362230  
; Patent No. 6352849  
; GENERAL INFORMATION:  
; APPLICANT: Tischfield, Jay A.  
; APPLICANT: Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide  
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences  
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide  
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &  
; ADDRESSEE: Russell PA  
; STREET: 200 East Broward Boulevard  
; CITY: Fort Lauderdale  
; STATE: FL  
; COUNTRY: USA  
; ZIP: 33301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/362,230  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/888,497  
; FILING DATE:  
; APPLICATION NUMBER: US 08/097,354  
; FILING DATE: 26-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Manso, Peter J.  
; REGISTRATION NUMBER: 32,264  
; REFERENCE/DOCKET NUMBER: IN21044-5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 305-527-2498  
; TELEFAX: 305-764-4996  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 124 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-362-230-39

Query Match 49.9%; Score 360.5; DB 4; Length 124;  
Best Local Similarity 55.6%; Pred. No. 1.3e-31;  
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY 1 NLVQGVMIKMTGK-SALQYNDYGCYGGSHWPVDQTDWCHADCCYGRLEKLGCE 59  
DB 1 NLVNFHRMIKLTGTGKEALSFGFYCHGCVGRGSPKDATDRCCVTHDCCYKLEKRGCG 60  
QY 60 PKLEKYLFSVSERGIFCAGRTTCQRLTCECDKRAALCFRRNLGTYNRKYAHYPNKLCTGP 119  
DB 61 TKFLSYKFSNGSRITCAKQDSCRSQLCECDKAAATCFARNKTTYNKYQYYSNKHCRGS 120

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QY 120 TPPC 123
Db 121 TPRC 124

RESULT 4
US-09-740-569-2
; Sequence 2, Application US/09740569
; Patent No. 6475484
; GENERAL INFORMATION:
; APPLICANT: Weiss, Jerrold
; APPLICANT: Elsbach, Peter
; APPLICANT: Liang, Ning-Sheng
; TITLE OF INVENTION: ANTIBACTERIAL GROUP IIA PHOSPHOLIPASE A2 AND METHODS OF USE THERE
; FILE REFERENCE: 5986/1E917US1
; CURRENT APPLICATION NUMBER: US/09/740,569
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: US 60/172,467
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 124
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-740-569-2

Query Match 49.9%; Score 360.5; DB 4; Length 124;
Best Local Similarity 54.8%; Pred. No. 1.3e-31;
Matches 68; Conservative 11; Mismatches 44; Indels 1; Gaps 1;

QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
Db 1 NLVNFHRLIKLTGKKAALSYGYGCHGCVGRGSPKDATDCCVTHDCCYKLEKRGCG 60

QY 60 PLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLGTYNRYKVAHPNKLCTGP 119
Db 61 TKLSYKFSNKSRIITCAKQDSQSCQLCECDKAAATCFARNKTYNKKYQYYSNKHCRGS 120

QY 120 TPPC 123
Db 121 TPRC 124

RESULT 5
PCT-US94-07926-39
; Sequence 39, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
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; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 124 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-07926-39

Query Match 49.9%; Score 360.5; DB 5; Length 124;
Best Local Similarity 55.6%; Pred. No. 1.3e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY 1 NLVQFGVMIEKMTGK-SALQYNDYGCYGGIGGSHWPVDQTDWCCHAHDCCYGRLEKLGCE 59
Db 1 NLVNFHRLIKLTGKKAALSYGYGCHGCVGRGSPKDATDCCVTHDCCYKLEKRGCG 60

QY 60 PLEKYLFSVSRGIFCAGRTTCORLTCECDKRAALCFRNLGTYNRYKVAHPNKLCTGP 119
Db 61 TKLSYKFSNKSRIITCAKQDSQSCQLCECDKAAATCFARNKTYNKKYQYYSNKHCRGS 120

QY 120 TPPC 123
Db 121 TPRC 124

RESULT 6
US-08-186-895-10
; Sequence 10, Application US/08186895
; Patent No. 5538885
; GENERAL INFORMATION:
; APPLICANT: Hollis, Melvyn
; APPLICANT: Needham, Maurice R.C.
; APPLICANT: Gooding, Clare
; APPLICANT: Grosveld, Franklin G.
; TITLE OF INVENTION: Expression Systems
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cushman, Darby & Cushman
; STREET: 1615 L Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/186,895
; FILING DATE: 27-JAN-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/046,383
; FILING DATE: 09-APR-1993
; APPLICATION NUMBER: US/07/810,414
; ATTORNEY/AGENT INFORMATION:
; NAME: Kokulis, Paul N.
; REGISTRATION NUMBER: 16,773
; REFERENCE/DOCKET NUMBER: PNK/3893/93802/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3000
; TELEFAX: 202-822-0944
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QY 1 NLUVGVGMIEKMTGK-SALQINDYCYGIGSGSHWPVDQTDWCHAHDCCYGRLEKLGCE 59
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Db 21 NLVNFHRMTKLTITGKEAALSYGFYCHGCVGGRGSPKDATDRCCVTHDCCYKLEKRGCG 80
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QY 60 PKLEKYLFSVSRBGIFFCAGRTTCORLTCEDCKRAALCFRNRLGTYNRKYAHYPNKLCTGP 119
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Db 81 TKFLSYKFSNSGRITCAKQDSCRSQLCEDCKAAATCFARNKITYNNKYQYYSNKHCRGS 140
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QY 120 TPFC 123
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Db 141 TPC 144
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RESULT 9
PCT-US94-07926-37
; Sequence 37, Application PC/TUS9407926
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 144 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-37

Query Match 49.9%; Score 360.5; DB 5; Length 144;
Best Local Similarity 55.6%; Pred. No. 1.5e-31;
Matches 69; Conservative 9; Mismatches 45; Indels 1; Gaps 1;

QY 1 NLUVGVGMIEKMTGK-SALQINDYCYGIGSGSHWPVDQTDWCHAHDCCYGRLEKLGCE 59
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 21 NLVNFHRMTKLTITGKEAALSYGFYCHGCVGGRGSPKDATDRCCVTHDCCYKLEKRGCG 80
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :

QY 60 PKLEKYLFSVSRBGIFFCAGRTTCORLTCEDCKRAALCFRNRLGTYNRKYAHYPNKLCTGP 119
   |||  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :  :
Db 81 TKFLSYKFSNSGRITCAKQDSCRSQLCEDCKAAATCFARNKITYNNKYQYYSNKHCRGS 140
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QY 120 TPFC 123
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Db 141 TPC 144
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Qy      120 TTPC 123
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Db      141 TPRC 144

RESULT 10
US-08-888-497-42
; Sequence 42, Application US/08888497
; Patent No. 5972677
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 125 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-888-497-42

Query Match          48.2%; Score 348; DB 2; Length 125;
Best Local Similarity 51.2%; Pred. No. 2.9e-30;
Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

Qy      1 NLVFGVMIEKMTGKSA-LQYNDYGCYCIGGGSHWPVDQTWCCHAHDCCYGRLEKLGCCE 59
       :::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 SLLEFGQMILFKTKRADVSYGFGYCHCGVGGRGSPKDATDWCCVTHTDCCYNRLKRGGC 60
                                     :::|||:|||||:|||||:|||||:|||||:|||||
Qy      60 PKLEKYLFSVSRGIFFCA-GRTTCORLTCECDKRAALCFRRNLGLTYNRKYAHYPNKLCTG 118
       :::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 TKFYTFYSFRGGQISGTNQDSCKRQLQCDDKAARCFARNKKSYLSLYQFYFNKFCKG 120
                                     :::|||:|||||:|||||:|||||:|||||:|||||
Qy      119 TPPEC 123
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Db      121 KTPSC 125

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5



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; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: US/08/888,497
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/651,405
; FILING DATE:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-888-497-35

Query Match 48.2%; Score 348; DB 2; Length 146;
Best Local Similarity 51.2%; Pred. No. 3.5e-30;
Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

QY 1 NLVQFGVMIEKMTGKSA-LQYNDYGCYCGIGGSHWPDQDWCCHAHDCYGRLEKLGCE 59
Db 22 SLLEFGOMILFKTKRADYSYGFYCHGCVGGSGPKDATDCCVTHDCCYNLEKRGCG 81
QY 60 PKLEKLYFSVSRGIFCA-GRITTCQRLTCECDKRAALCFRNLGTNRYKIAHYPNKLTG 118
Db 82 TKFVTYKFSYRGQIISCSNTQDSCRQLQCQDKAAAECPARNKKSYSLYQYFYPNFKCG 141
QY 119 PTPPC 123
Db 142 KTFSC 146

RESULT 14
US-09-362-230-35
; Sequence 35, Application US/09362230
; Patent No. 6352849
; GENERAL INFORMATION:
; APPLICANT: Tischfield, Jay A.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Mammalian Phospholipase A2 Nucleotide
; TITLE OF INVENTION: Sequences and Low Molecular Weight Amino Acid Sequences
; TITLE OF INVENTION: Encoded Thereby, Antisense Sequences and Nucleotide
; TITLE OF INVENTION: Sequences Having Internal Ribosome Binding Sites
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell PA
; STREET: 200 East Broward Boulevard
; CITY: Fort Lauderdale
; STATE: FL
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; APPLICATION NUMBER: PCT/US94/07926
; FILING DATE: 15-JUL-1994
; CLASSIFICATION:

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/097,354
; FILING DATE: 26-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: IN21044-5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305-527-2498
; TELEFAX: 305-764-4996
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-07926-35

Query Match      48.2%; Score 348; DB 5; Length 146;
Best Local Similarity 51.2%; Pred. No. 3.5e-30;
Matches 64; Conservative 14; Mismatches 45; Indels 2; Gaps 2;

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Qy      60 PKLEKYLFSVSERGIFCA-GRITTCQRLTCECDKRAALCFRRNLGTYNRYAHYPNKLCTG 118
Db      82 TKFVTKESYRGQISCSSTNQDSCKQLCCDDKAAECFARNKKSYSLSKYQFYFNKECKG 141
Qy      119 PTPPC 123
Db      142 KTPSC 146
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Search completed: July 3, 2004, 05:18:47  
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